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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:34:18 ; Search time 104.746 Seconds
(without alignments)
73.847 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139
Perfect score: 100
Sequence: 1 LLVVPARKDYGSQEDFTQV 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	20	4	AAM01172 Human pro
2	100	100.0	20	4	AAU69817 Human pro
3	100	100.0	20	4	AAG99057 Human pro
4	100	100.0	20	4	ABU71708 Prostata
5	100	100.0	20	5	ABB95277 Epitope m
6	100	100.0	20	6	ABR54389 Prostata
7	100	100.0	20	7	ADB13972 Human pro
8	100	100.0	20	7	ADG26388 Human pro
9	100	100.0	108	2	AAV11883 Human 5'
10	100	100.0	126	2	AAV35991 Extended
11	100	100.0	126	8	ADP19299 Human sec
12	100	100.0	172	7	ADD69590 Human REM
13	100	100.0	174	8	ADP81123 Protein o
14	100	100.0	214	8	ADR65994 Human pro
15	100	100.0	214	8	ADR66892 Human pro
16	100	100.0	233	2	AAW75060 Human sec
17	100	100.0	233	6	ABQ01936 Novel hum
18	100	100.0	240	4	AAQ62153 Human P50
19	100	100.0	240	5	ABB89113 Human pol
20	100	100.0	241	2	AAW69386 Prostata
21	100	100.0	241	2	AAW59954 Amino aci
22	100	100.0	241	2	AAW71870 Amino aci
23	100	100.0	241	2	AAW58380 Human sec
24	100	100.0	241	3	AAW82003 Human imm
25	100	100.0	241	3	ABG94412 Human pro

26	100	100.0	241	4	AAM01118 Human pro
27	100	100.0	241	4	AAU69764 Human pro
28	100	100.0	241	4	AAU74801 Prostata
29	100	100.0	241	4	AAG99003 Human pro
30	100	100.0	241	4	ABU71654 Prostata
31	100	100.0	241	4	AAU04962 Human ARA
32	100	100.0	241	4	ABG96434 Human ova
33	100	100.0	241	5	ABG95223 Human N1-
34	100	100.0	241	5	ABG76666 Prostata
35	100	100.0	241	5	ABR54335 Prostata
36	100	100.0	241	6	ABR54335 Prostata
37	100	100.0	241	7	ADB75601 Prostata
38	100	100.0	241	7	ADB13564 Human pro
39	100	100.0	241	7	ADG25980 Human pro
40	100	100.0	241	7	ADN39286 Cancer/an
41	100	100.0	258	5	ABG96433 Human ova
42	100	100.0	258	7	ADB75599 Prostata
43	100	100.0	273	2	AAW61618 Clone HPW
44	100	100.0	273	7	ABW01500 Human rec
45	84	84.0	241	5	ABB09512 Human TSP

ALIGNMENTS

RESULT 1
AAM01172
ID AAM01172 standard; peptide; 20 AA.
XX AC AAM01172;
XX XX
DT 04-OCT-2001 (first entry)
DE Human prostate-specific peptide used in epitope mapping studies #29.
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytotatic; gene therapy; metastasis.
XX Homo sapiens.
XX PN W0200151633-A2.
XX PD 19-JUL-2001.
XX PF 16-JAN-2001; 2001WO-US001574.
XX PR 14-JAN-2000; 2000US-00483672.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XX Wang A, Meagher MJ;
XX WPI; 2001-425873/45.
XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
XX vaccines.
XX Claim 2; Page 403; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used to treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate

CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
 CC polynucleotide and amino acid sequences used in the exemplification of
 CC the present invention

XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSQEDFTQV 20
 |||||
 DB 1 LLVVPAAKKDYGSQEDFTQV 20

RESULT 2
 AAU69817
 ID AAU69817 standard; peptide; 20 AA.
 XX
 AC AAU69817;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE Human prostate protein P703P antigenic epitope #14.
 XX
 DE Human; prostate cancer; ss; cytostatic; immunostimulant; tumour; antigen;
 XX
 KW epitope.
 XX
 KW Homo sapiens.
 XX
 OS WO200173032-A2.
 XX
 PN 04-OCT-2001.
 XX
 PD 27-MAR-2001; 2001WO-US009919.
 XX
 PF 27-MAR-2001; 2000US-00536857.
 XX
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 WPI; 2001-639232/73.
 XX
 XX New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer.
 PT
 PS Claim 2; Page 404; 579pp; English.
 XX
 XX The invention relates to isolated prostate-specific polynucleotides,
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised
 CC against the polypeptides (or antigenic epitopes derived from them) and
 CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific peptide of the invention. The peptides either represent

CC antigenic epitopes or domains of prostate specific proteins
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSQEDFTQV 20
 |||||
 DB 1 LLVVPAAKKDYGSQEDFTQV 20

RESULT 3
 AAG99057
 ID AAG99057 standard; peptide; 20 AA.
 XX
 AC AAG99057;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human prostate-specific epitope mapping peptide #29.
 XX
 DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
 KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
 KW prostate specific antigen; PSA.
 XX
 OS Homo sapiens.
 XX
 PN WO200134802-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 09-NOV-2000; 2000WO-US030904.
 XX
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
 XX
 WPI; 2001-308785/32.
 XX
 XX Isolated polypeptide comprising at least an immunogenic portion of a
 PT prostate-specific protein, useful in the diagnosis and therapy of
 PT prostate cancer.
 PT
 PS Claim 3; Page 303; 325pp; English.
 XX
 XX The present invention describes an isolated polypeptide (P1) comprising
 CC at least an immunogenic portion of a prostate-specific protein, or its
 CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
 CC (N1) have cytostatic activity and can be used in vaccine production. The
 CC polypeptides, nucleic acids and antibodies from the present invention are
 CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
 CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
 CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
 CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
 CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
 CC and polypeptide sequences used in the exemplification of the present
 CC invention

XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 100; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSQEDFTQV 20
 |||||
 DB 1 LLVVPAAKKDYGSQEDFTQV 20

CC prostate cancer therapy associated peptide. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?docID=US20020192763

XX ABU71708 standard; peptide; 20 AA.

XX AC ABU71708;

XX DT 10-JUN-2003 (first entry)

XX DE Prostate cancer therapy associated peptide #30.

XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA.

XX OS Homo sapiens.

XX PN US2002192763-A1.

XX PD 19-DEC-2002.

XX PF 29-JUN-2001; 2001US-00895793.

XX PR 04-OCT-1999; 99US-0157455P.

XX PR 04-OCT-2000; 2000US-00679272.

XX PR 28-MAR-2001; 2001US-00822827.

XX PA (XUJJ/) XU J.

XX PA (DILL/) DILLON D C.

XX PA (MITC/) MITCHAM J L.

XX PA (HARL/) HARLOCKER S L.

XX PA (JIAN/) JIANG Y.

XX PA (KALO/) KALOS M D.

XX PA (FANG/) FANGER G R.

XX PA (RETT/) RETTER M W.

XX PA (STOL/) STOLK J A.

XX PA (DAYC/) DAY C H.

XX PA (VEDV/) VEDVICK T S.

XX PA (CART/) CARTER D.

XX PA (LISX/) LI S X.

XX PA (WANG/) WANG A.

XX PA (SKEI/) SKEIKY Y A W.

XX PA (HEPL/) HEPLER W T.

XX PA (HEND/) HENDERSON R A.

XX PA (HURA/) HURAL J.

XX PA (MCNE/) MCNEILL P D.

XX PA (HOUG/) HOUGHTON R L.

XX PA (DBAS/) Y DE BASSOLS C V.

XX PA (FOYT/) FOY T M.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;

PI Mcneill PD, Houghton RL, Y De Bassols CV, Foy TM;

XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the

FT treatment and diagnosis of prostate cancer.

XX Example 18; SEQ ID NO 522; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino

CC acid sequence of immunogenic portions of any of the 3 sequences not

CC defined in the specification, or sequences having at least 70 or 90 %

CC sequence identity to any one of the 35 sequences defined in the USPTO web

CC site, which is encoded by any of the 4 nucleotide sequences not defined

CC in the specification. The fusion protein, composition and methods are

CC useful for diagnosing, preventing and/or treating cancer, particularly

CC prostate cancer. The proteins are useful as markers to indicate the

CC presence or absence of cancer. This is the amino acid sequence of a

CC Query Match 100.0%; Score 100; DB 4; Length 20;
CC Best Local Similarity 100.0%; Pred. No. 1.3e-09;
CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ Sequence 20 AA;

QY 1 LLVVPALKKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 LLVVPALKKDYGSQEDFTQV 20
| | | | | | | | | | | | | | | | | | | | | |

RESULT 5
ABB95277
ID ABB95277 standard; peptide; 20 AA.

XX AC ABB95277;

XX DT 19-JUL-2002 (first entry)

XX DE Epitope mapping study peptide SEQ ID NO 522.

XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy.

XX OS Unidentified.

XX PN US2002022248-A1.

XX PD 21-FEB-2002.

XX PF 12-JAN-2001; 2001US-00759143.

XX PR 25-FEB-1997; 97US-00806099.

XX PR 01-AUG-1997; 97US-00904804.

XX PR 10-FEB-1998; 98US-0020956.

XX PR 25-FEB-1998; 98US-0030607.

XX PR 14-JUL-1998; 98US-00115453.

XX PR 23-SEP-1998; 98US-00159812.

XX PR 15-JAN-1999; 99US-00232149.

XX PR 09-APR-1999; 99US-00288946.

XX PR 13-JUL-1999; 99US-00352616.

XX PR 12-NOV-1999; 99US-00439313.

XX PR 18-NOV-1999; 99US-00443686.

XX PR 14-JAN-2000; 2000US-00483672.

XX PR 27-MAR-2000; 2000US-00536857.

XX PR 09-MAY-2000; 2000US-00568100.

XX PR 12-MAY-2000; 2000US-00570737.

XX PR 13-JUN-2000; 2000US-00593793.

XX PR 27-JUN-2000; 2000US-00605783.

XX PR 10-AUG-2000; 2000US-00636215.

XX PR 29-AUG-2000; 2000US-00651236.

XX PR 06-SEP-2000; 2000US-00657279.

XX PR 02-OCT-2000; 2000US-00679426.

XX PR 10-OCT-2000; 2000US-00685166.

XX PA (XUJJ/) XU J.

XX PA (DILL/) DILLON D C.

XX PA (MITC/) MITCHAM J L.

XX PA (HARL/) HARLOCKER S L.

XX PA (JIAN/) JIANG Y.

XX PA (KALO/) KALOS M D.

XX PA (FANG/) FANGER G R.

XX PA (RETT/) RETTER M W.

XX PA (STOL/) STOLK J A.

XX PA (DAYC/) DAY C H.

XX PA (VEDV/) VEDVICK T S.

XX PA (CART/) CARTER D.

XX PA (LISX/) LI S X.

PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 522; 87pp; English.
PS
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC peptide described in the invention
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 100; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVPAAIKDYGSGEDFTQV 20
Db 1 LLVVPAAIKDYGSGEDFTQV 20
RESULT 6
ABR54389
ID ABR54389 standard; protein; 20 AA.
XX
XX ABR54389;
AC
XX
XX 28-AUG-2003 (first entry)
DT
XX
XX Prostate tumour specific related peptide for epitope mapping SEQ ID 522.
DE
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX immune response; prostate cancer.
XX
XX Homo sapiens.
XX
XX WO200289747-A2.
PN
XX
XX 14-NOV-2002.
PD
XX
XX 09-MAY-2002; 2002WO-US014753.
PF
XX
XX 09-MAY-2001; 2001US-00852911.
PR
XX 29-JUN-2001; 2001US-00895814.
PR
XX 10-DEC-2001; 2001US-00012896.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX

PS Example 18; Page 470-471; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 100; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVPAAIKDYGSGEDFTQV 20
Db 1 LLVVPAAIKDYGSGEDFTQV 20
RESULT 7
ADB13972
ID ADB13972 standard; peptide; 20 AA.
XX
XX ADB13972;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human prostate protein P503S epitope mapping peptide #2099.
DE
XX
XX Human; prostate specific CDNA; cytostatic; immunostimulant; gene therapy;
XX cell therapy; vaccine; T-cell epitope;
XX class I major histocompatibility complex allele; MHC; prostate cancer;
XX tumour; antigen presenting cell; epitope.
XX
XX Homo sapiens.
XX
XX US2003185830-A1.
PN
XX
XX 02-OCT-2003.
PD
XX
XX 12-NOV-2002; 2002US-00294025.
PF
XX
XX 25-FEB-1997; 97US-00806099.
PR
XX 01-AUG-1997; 97US-00904804.
PR
XX 09-FEB-1998; 98US-00020956.
PR
XX 25-FEB-1998; 98US-00030607.
PR
XX 14-JUL-1998; 98US-00115453.
PR
XX 23-SEP-1998; 98US-00159812.
PR
XX 15-JAN-1999; 99US-00232149.
PR
XX 09-APR-1999; 99US-00288946.
PR
XX 13-JUL-1999; 99US-00352616.
PR
XX 12-NOV-1999; 99US-00439313.
PR
XX 18-NOV-1999; 99US-00443686.
PR
XX 14-JAN-2000; 2000US-00483672.
PR
XX 27-MAR-2000; 2000US-00536857.
PR
XX 09-MAY-2000; 2000US-00568100.
PR
XX 12-MAY-2000; 2000US-00570737.
PR
XX 13-JUN-2000; 2000US-00593793.
PR
XX 27-JUN-2000; 2000US-00605783.
PR
XX 09-AUG-2000; 2000US-00636215.
PR
XX 29-AUG-2000; 2000US-00651236.
PR
XX 06-SEP-2000; 2000US-00657279.
PR
XX 02-OCT-2000; 2000US-00679426.
PR
XX 10-OCT-2000; 2000US-00685166.
PR
XX 09-NOV-2000; 2000US-00709729.
PR
XX 12-JAN-2001; 2001US-00759143.
PR
XX 09-FEB-2001; 2001US-00780669.
PR
XX 09-MAY-2001; 2001US-00852911.
PR
XX 29-JUN-2001; 2001US-00895814.
PR
XX 10-DEC-2001; 2001US-00012896.
PR
XX 09-MAY-2002; 2002US-00144678.
XX

PA (CORI-) CORIXA CORP.
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
DR
XX New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
XX Example 18; Page; 101pp; English.
PS
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB1356, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is an epitope or
CC peptide derived from one of the prostate specific proteins of the
CC invention. Note: Except where otherwise indicated, the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 100; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;
Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 1 LLVVPAlKKDYGSQEDFTQV 20
RESULT 8
ADG26388
ID ADG26388 standard; peptide; 20 AA.
XX AC ADG26388;
XX XX 26-FEB-2004 (first entry)
XX DE Human prostate-specific polypeptide #58.
XX KW Human; prostate-specific polypeptide; prostate cancer; cytostatic.
XX OS Homo sapiens.

XX PN US2003157089-A1.
XX PD 21-AUG-2003.
XX PF 09-MAY-2002; 2002US-00144678.
XX PR 25-FEB-1997; 97US-00806099.
XX PR 01-AUG-1997; 97US-00904804.
XX PR 09-FEB-1998; 98US-00020956.
XX PR 25-FEB-1998; 98US-00030607.
XX PR 14-JUL-1998; 98US-00115453.
XX PR 23-SEP-1998; 98US-00159812.
XX PR 15-JAN-1999; 99US-00232149.
XX PR 09-APR-1999; 99US-00288946.
XX PR 13-JUL-1999; 99US-00352616.
XX PR 12-NOV-1999; 99US-00439313.
XX PR 18-NOV-1999; 99US-00443686.
XX PR 14-JAN-2000; 2000US-00483672.
XX PR 27-MAR-2000; 2000US-00536857.
XX PR 09-MAY-2000; 2000US-00568100.
XX PR 12-MAY-2000; 2000US-00570737.
XX PR 13-JUN-2000; 2000US-00593793.
XX PR 27-JUN-2000; 2000US-00605783.
XX PR 09-AUG-2000; 2000US-00636215.
XX PR 29-AUG-2000; 2000US-00651236.
XX PR 06-SEP-2000; 2000US-00657279.
XX PR 10-OCT-2000; 2000US-00679426.
XX PR 10-OCT-2000; 2000US-00685166.
XX PR 09-NOV-2000; 2000US-00709729.
XX PR 12-JAN-2001; 2001US-00759143.
XX PR 09-FEB-2001; 2001US-00780669.
XX PR 09-MAY-2001; 2001US-00852911.
XX PR 29-JUN-2001; 2001US-00895814.
XX PR 10-DEC-2001; 2001US-00012896.
XX PA (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hurai J;
XX McNeill PD, Houghton RL, Vinals Y De Bassolec, Foy TM, Watanabe Y;
XX Mesgher WJ, Deng T;
XX WPI; 2003-777973/73.
XX New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
XX Example 18; SEQ ID NO 522; 99pp; English.
PS The invention relates to human prostate-specific polypeptides and the
XX polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents a human prostate-specific polypeptide of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 100; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVPAlKKDYGSQEDFTQV 20

Db 1 LLVWPAIKKDYGSQEDFTQV 20

RESULT 9
AAV11883
ID AAV11883 standard; protein; 108 AA.
XX
AC AAV11883;
XX
XX 18-JUN-1999 (first entry)
XX
XX Extended human secreted protein sequence, SEQ ID NO. 483.
XX
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide; prostate;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokine; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition.
XX
XX Homo sapiens.
XX
XX WO9906550-A2.
XX
XX 11-FEB-1999.
XX
XX 31-JUL-1998; 98WO-IB001232.
XX
XX 01-AUG-1997; 97US-00905144.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
XX WPI; 1999-153780/13.
XX
XX N-PSDB; AAX40605.
XX
XX New isolated prostate-derived nucleic acids - used to develop products
XX which may have cytokine, immune regulatory, haematopoiesis regulating,
XX anti-inflammatory or tumour inhibition activity.
XX
XX Claim 34; Page 605; 675pp; English.
XX
XX AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
XX human secreted proteins expressed in prostate, and encode the proteins
XX given in AAV1176 to AAV1193 respectively. The proteins given represent
XX the signal peptide and an N-terminal fragment of a secreted protein. The
XX nucleic acid sequences can be used for producing secreted human gene
XX products. They can also be used to develop products for diagnosis and
XX therapy. The proteins obtained may have cytokine activity, cell
XX proliferation and differentiation activity, haematopoiesis regulating
XX activity, tissue growth regulating activity, reproductive hormone
XX regulating activity, chemotactic/chemokinetic activity, haemostatic and
XX thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, tumour inhibition activity or other activities. The products
XX can be used in forensic, gene therapy and chromosome mapping procedures.
XX The sequences can also be used for obtaining corresponding promoter
XX sequences. The nucleic acids encoding the signal peptides can be used for
XX directing extracellular secretion of a polypeptide or the insertion of a
XX polypeptide into a membrane, or importing a polypeptide into a cell
XX
XX Sequence 108 AA;
XX
XX Query Match 100.0%; Score 100; DB 2; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 9.2e-09;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LLVWPAIKKDYGSQEDFTQV 20
XX
XX 70 LLVWPAIKKDYGSQEDFTQV 89
XX

Db 1 LLVWPAIKKDYGSQEDFTQV 20

RESULT 10
AAV35991
ID AAV35991 standard; protein; 126 AA.
XX
AC AAV35991;
XX
XX 13-SEP-1999 (first entry)
XX
XX Extended human secreted protein sequence, SEQ ID NO. 240.
XX
XX Secreted protein; human; cytokine; cellular proliferation; cell movement;
XX cellular differentiation; immune system regulator; anti-inflammatory;
XX haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
XX reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
XX genetic disease.
XX
XX Homo sapiens.
XX
XX WO9931236-A2.
XX
XX 24-JUN-1999.
XX
XX 17-DEC-1998; 98WO-IB002122.
XX
XX 17-DEC-1997; 97US-0069957P.
XX 09-FEB-1998; 98US-0074121P.
XX 13-APR-1998; 98US-0081563P.
XX 10-AUG-1998; 98US-0096118P.
XX
XX (GEST) GENSET.
XX
XX Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
XX WPI; 1999-385906/32.
XX
XX N-PSDB; AAX97675.
XX
XX New isolated human secreted proteins.
XX
XX Claim 9; Page 267-268; 516pp; English.
XX
XX This sequence is encoded by an extended human secreted protein coding
XX sequence of the invention. The secreted proteins can be used in treating
XX or controlling a variety of human conditions. The secreted proteins may
XX act as cytokines or may affect cellular proliferation or differentiation
XX or may act as immune system regulators, haematopoiesis regulators, tissue
XX growth regulators, regulators of reproductive hormones or cell movement
XX or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
XX tumour inhibition activity. The DNAs can be used in forensic procedures
XX to identify individuals or in diagnostic procedures to identify
XX individuals having genetic diseases resulting from abnormal expression of
XX the genes corresponding to the extended cDNAs. They are also useful for
XX constructing a high resolution map of the human chromosomes. They can
XX also be used for gene therapy to control or treat genetic diseases
XX
XX Sequence 126 AA;
XX
XX Query Match 100.0%; Score 100; DB 2; Length 126;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-08;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LLVWPAIKKDYGSQEDFTQV 20
XX
XX 70 LLVWPAIKKDYGSQEDFTQV 89
XX

Db 1 LLVWPAIKKDYGSQEDFTQV 20

RESULT 11
ADP19299
ID ADP19299 standard; protein; 126 AA.
XX
AC ADP19299;
XX
XX 26-AUG-2004 (first entry)
XX
XX

```
DE Human secreted polypeptide #150.
KW Human; secreted protein; genetic disease.
XX Homo sapiens.
OS
XX
XX US2004110939-A1.
PN
XX
XX 10-JUN-2004.
PD
XX
XX 15-OCT-2001; 2001US-00978360.
PF
XX
XX 17-DEC-1998; 98WO-IB002122.
PR
XX 09-FEB-1999; 99WO-IB000282.
PR
XX 21-JUN-2000; 2000WO-IB000951.
PR
XX 15-SEP-2000; 2000US-00663600.
PR
XX
XX (GEST ) GENSET SA.
PA
XX
XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
PI Duclert A;
PI
PI WPI; 2004-440404/41.
DR N-PSDB; ADP18894.
DR
XX
XX New isolated polynucleotide encoding secreted polypeptide, useful for
PT gene therapy, or in diagnostic procedures to identify individuals having
PT genetic diseases resulting from abnormal expression of the genes.
PT
XX
XX Claim 2; SEQ ID NO 555; 113pp; English.
PS
XX
XX The invention relates to human cDNA sequences that encode human secreted
CC proteins. The invention also relates to an antibody that specifically
CC binds to a polypeptide of the invention and a method of binding the
CC polypeptide to an antibody. The polynucleotides are useful for expressing
CC the entire secreted proteins which they encode and for distinguishing
CC human tissues and cells from non-human tissues and cells, and for
CC distinguishing between human tissues and cells that do or do not express
CC the polynucleotides comprising the cDNAs. The polynucleotides and
CC polypeptides are useful in forensic procedures or diagnostic procedures
CC to identify individuals with genetic diseases resulting from abnormal
CC expression of the genes corresponding to the cDNAs. The sequences are
CC also useful in gene therapy to control or treat genetic diseases. This
CC sequence represents a human secreted polypeptide of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
CC
XX
XX SQ Sequence 126 AA;
Query Match 100.0%; Score 100; DB 8; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVVPAIKKDYGSQEDFTQV 20
Db 70 LLVVVPAIKKDYGSQEDFTQV 89
RESULT 12
ADD69590
ID ADD69590 standard; protein; 172 AA.
XX
XX AC ADD69590;
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Human REMAP protein - SEQ ID 19.
DE
XX
XX human; receptor and membrane-associated protein; REMAP; cytostatic;
KW antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
KW cerebroprotective; anti-HIV; anti-allergic; anti-inflammatory;
KW thyromimetic; cell proliferative; cancer; atherosclerosis; neurological;
```

```
KW epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS;
KW allergy; developmental; hypothyroidism; Cushing's syndrome; infection.
XX
OS Homo sapiens.
XX
XX WO2003048305-A2.
PN
XX
XX 12-JUN-2003.
PD
XX
XX 13-NOV-2002; 2002WO-US036759.
PF
XX
XX 13-NOV-2001; 2001US-0333097P.
PR
XX 15-NOV-2001; 2001US-0335274P.
PR
XX 14-DEC-2001; 2001US-0340542P.
PR
XX 18-DEC-2001; 2001US-0342166P.
PR
XX 11-JAN-2002; 2002US-0347580P.
PR
XX 14-JAN-2002; 2002US-0348687P.
PR
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y;
PI Chawla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM;
PI Thangavelu K, Lee S, Emerling BM, Kable AE, Khare R, Baughn MR;
PI Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Forsythe LJ;
PI Lee EA, Swarnakar A, Kallick DA, Griffin JA, Elliott VS, Gorvad AE;
PI Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U;
PI Burrill JD, Blake JJ, Ho A, Zheng W, Gao J;
PI
XX WPI; 2003-513744/48.
DR N-PSDB; ADD69637.
DR
XX
XX New human receptors and membrane-associated proteins (REMAP), useful for
PT diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
PT infections.
PT
XX
XX Claim 1; SEQ ID NO 19; 298pp; English.
PS
XX
XX The invention relates to a novel isolated polypeptide comprising a human
CC receptor and membrane-associated protein (REMAP). The polypeptide of the
CC invention demonstrates cytostatic, antiarteriosclerotic, anticonvulsant,
CC neurotropic, neuroprotective, cerebroprotective, anti-HIV, anti-allergic,
CC anti-inflammatory and thyromimetic activities and may be useful for
CC treating and diagnosing various disorders including those which are cell
CC proliferative such as cancer and atherosclerosis, neurological including
CC epilepsy, Huntington's disease and stroke, immune/inflammatory
CC particularly AIDS and allergies and developmental such as hypothyroidism
CC and Cushing's syndrome, as well as infections. The current sequence is
CC that of the human REMAP protein of the invention.
CC
XX
XX SQ Sequence 172 AA;
Query Match 100.0%; Score 100; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVVVPAIKKDYGSQEDFTQV 20
Db 51 LLVVVPAIKKDYGSQEDFTQV 70
RESULT 13
ADP81123
ID ADP81123 standard; protein; 174 AA.
XX
XX AC ADP81123;
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Protein of human ovarian specific gene, SEQ ID No 157.
DE
XX
XX normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
KW metastatic; cancer; vaccine; cytostatic; human.
```

XX OS Homo sapiens.
XX KW WO2004053079-A2.
XX PD 24-JUN-2004.
XX PF 08-DEC-2003; 2003WO-US038855.
XX PR 06-DEC-2002; 2002US-0431301P.
XX PR 06-DEC-2002; 2002US-0431321P.
XX PR 30-JUN-2003; 2003US-0484584P.
XX PR 07-NOV-2003; 2003US-0518607P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;
XX DR WPI; 2004-468850/44.
XX DR N-PSDB; ADP80988.
XX PT New ovarian specific nucleic acid molecules and polypeptides useful for
XX FT diagnosing, preventing or treating ovarian cancer, for producing
XX PT transgenic animals or cells, or for research purposes.
XX PS Claim 12; SEQ ID NO 157; 754pp; English.
XX CC The invention relates to novel isolated nucleic acid molecules and
XX CC polypeptides present in normal and neoplastic ovarian cells. These
XX CC comprise a nucleic acid sequence encoding any of the 167 amino acid
XX CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
XX CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
XX CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
XX CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
XX CC further comprises: a method for determining the presence of an ovarian
XX CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
XX CC nucleic acid molecule; a host cell comprising the vector; a method for
XX CC producing a polypeptide encoded by the above nucleic acid molecule; a
XX CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
XX CC or its fragment that specifically binds to the above polypeptide; a
XX CC method for determining the presence of an ovarian specific protein in a
XX CC sample; a method for diagnosing or monitoring the presence and metastases
XX CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
XX CC presence of cancer in a patient; the kit comprising a means for
XX CC determining the presence of the above nucleic acid molecule or
XX CC polypeptide; a method of treating a patient with ovarian cancer; and a
XX CC vaccine comprising the above polypeptide or nucleic acid encoding the
XX CC polypeptide. The isolated nucleic acid molecules and polypeptides have
XX CC cytostatic activity. The isolated polypeptides may be used to create a
XX CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
XX CC for diagnosing or monitoring the presence and metastases of ovarian
XX CC cancer and treating ovarian cancer. This sequence represents the protein
XX CC of an ovarian specific gene of the invention.
XX PS Sequence 174 AA;
XX FT Query Match 100.0%; Score 100; DB 8; Length 174;
XX FT Best Local Similarity 100.0%; Pred. No. 1.6e-08;
XX FT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVVPALKDYGSQEDFTQV 20
DB 8 LLVVPALKDYGSQEDFTQV 27
|||||
RESULT 14
ADR65994
ID ADR65994 standard; protein; 214 AA.
XX AC ADR65994;
XX DT 02-DEC-2004 (first entry)
XX PS 1 LLVVPALKDYGSQEDFTQV 20
|||||
Query Match 100.0%; Score 100; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVVPALKDYGSQEDFTQV 20
|||||

DE XX Human prostatic carcinoma derived protein SEQ ID 190 #1.
XX KW human; cytostatic; diagnosis; prostatic cancer;
XX OS differential expression analysis.
XX OS Homo sapiens.
XX PN WO2004076614-A2.
XX PD 10-SEP-2004.
XX PF 22-FEB-2004; 2004WO-DE000433.
XX PR 27-FEB-2003; 2003DE-01009985.
XX PR 14-MAY-2003; 2003DE-01022134.
XX PA (HINZ/) HINZMANN B.
XX PA (DAHL/) DAHL E.
XX PA (ROSE/) ROSENTHAL A.
XX PA (HERM/) HERMANN K.
XX PA (PILA/) PILARSKY C.
XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
XX PI Schmitt A, Beckmann G, Bruemendorf T, Kinneemann H, Roepcke S;
XX PI Xinzhang L, Staub E;
XX DR WPI; 2004-653386/63.
XX FT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
XX FT useful for diagnosis, treatment and in screening for specific binding
XX FT agents.
XX PS Claim 2; Page 585; 1607pp; German.
XX CC This invention describes novel cytostatic polynucleotide and polypeptide
XX CC sequences which can be used in a method for diagnosing prostatic cancer
XX CC or the risk of developing prostatic cancer. Diagnosis is based on
XX CC determining over transcription or over expression of the sequences in
XX CC prostatic tissue. Screening for inhibitors of the sequences or detection
XX CC substances involves a binding assay, any compounds that bind are
XX CC selected, optionally after deconvolution of mixtures. Detection of a
XX CC predetermined minimum level of the reporter indicates the presence of
XX CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
XX CC short-interfering RNA or ribozymes; an organic molecule of molecular
XX CC weight below 5000, preferably 300, that binds to the polypeptide; an
XX CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
XX CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
XX CC (monoclonal) antibody directed against Ab or any of the above derivatised
XX CC with a reporter group, cell toxin, immunostimulatory molecules and/or
XX CC radioisotope. The polynucleotides are identified in human prostatic
XX CC cancer by differential expression analysis, using DNA microarrays,
XX CC between normal and tumorous tissues, with (over)expression being detected
XX CC by quantitative PCR. Analysis of prostatic cancer samples showed that
XX CC CD24 was upregulated in many of them. Sections of tissue, isolated from
XX CC prostatic cancer patients, or subjects at risk, were incubated
XX CC sequentially with anti-human CD4 murine monoclonal antibodies;
XX CC biotinylated second antibody; streptavidin-conjugated horseradish
XX CC peroxidase and then diaminobenzidine as colour former (brown). The
XX CC samples were counterstained with hemalum (blue). Malignant cells stained
XX CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
XX CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
XX CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
XX CC polynucleotide and polypeptide sequences used in the method of the
XX CC invention.
XX PS Sequence 214 AA;
XX FT Query Match 100.0%; Score 100; DB 8; Length 214;
XX FT Best Local Similarity 100.0%; Pred. No. 2e-08;
XX FT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLVVPALKDYGSQEDFTQV 20
|||||

Db 93 LLVVPAlKKDYGSQEDFTQV 112

RESULT 15

ADR66892

ID ADR66892 standard; protein; 214 AA.

XX AC ADR66892;

XX DT 02-DEC-2004 (first entry)

XX DE Human prostatic carcinoma derived DNA SEQ ID 190 #4.

XX KW human; cytostatic; diagnosis; prostatic cancer;

XX KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.

XX PR 27-FEB-2003; 2003DE-01009985.

XX PR 14-MAY-2003; 2003DE-01022134.

XX PA (HINZ/) HINZMANN B.

XX PA (DAHL/) DAHL E.

XX PA (ROSE/) ROSENTHAL A.

XX PA (HERM/) HERMANN K.

XX PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;

XX PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;

XX PI Xinzhang L, Staub E;

XX DR WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,

XX useful for diagnosis, treatment and in screening for specific binding

XX agents.

XX Claim 2; Page 1545; 1607pp; German.

XX This invention describes novel cytostatic polynucleotide and polypeptide

XX sequences which can be used in a method for diagnosing prostatic cancer

XX or the risk of developing prostatic cancer. Diagnosis is based on

XX determining over transcription or over expression of the sequences in

XX prostatic tissue. Screening for inhibitors of the sequences or detection

XX substances involves a binding assay, any compounds that bind are

XX selected, optionally after deconvolution of mixtures. Detection of a

XX predetermined minimum level of the reporter indicates the presence of

XX tumour cells. Inhibitors can be chosen from antisense oligonucleotides,

XX short-interfering RNA or ribozymes; an organic molecule of molecular

XX weight below 5000, preferably 300, that binds to the polypeptide; an

XX aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the

XX polypeptide, preferably humanised or human; an anti-idiotypic, non-human

XX (monoclonal) antibody directed against Ab or any of the above derivatised

XX with a reporter group, cell toxin, immunostimulatory molecules and/or

XX radioisotope. The polynucleotides are identified in human prostatic

XX cancer by differential expression analysis, using DNA microarrays,

XX between normal and tumorous tissues, with (over)expression being detected

XX by quantitative PCR. Analysis of prostatic cancer samples showed that

XX CD24 was upregulated in many of them. Sections of tissue, isolated from

XX prostatic cancer patients, or subjects at risk, were incubated

XX sequentially with anti-human CD4 murine monoclonal antibodies;

XX biotinylated second antibody; streptavidin-conjugated horseradish

XX peroxidase and then diaminobenzidine as colour former (brown). The

XX samples were counterstained with hemalum (blue). Malignant cells stained

XX strongly but non-malignant cells only weakly. In 15 of 63 samples of

XX adenocarcinoma, membrane and cytoplasmic staining was very strong, and

XX lymph node metastases were also stained. ADR65805-ADR66954 represent the

CC polynucleotide and polypeptide sequences used in the method of the

CC invention.

XX

SQ Sequence 214 AA;

Query Match 100.0%; Score 100; DB 8; Length 214;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20

Db 93 LLVVPAlKKDYGSQEDFTQV 112

Search completed: February 5, 2005, 19:59:54

Job time : 107.746 secs

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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:50:20 ; Search time 25.4237 Seconds
(without alignments)
58.724 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139

Perfect score: 100

Sequence: 1 LLVVPALIKDYGSGEDFTQV 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	20	3	US-09-439-313-522
2	100	100.0	20	4	US-09-636-215-522
3	100	100.0	20	4	US-09-685-166A-522
4	100	100.0	20	4	US-09-679-426-522
5	100	100.0	20	4	US-09-759-143-522
6	100	100.0	20	4	US-09-651-236-522
7	100	100.0	233	4	US-09-148-545-137
8	100	100.0	241	3	US-08-808-148-1
9	100	100.0	241	3	US-09-020-956-114
10	100	100.0	241	3	US-09-030-607-114
11	100	100.0	241	3	US-09-439-313-114
12	100	100.0	241	3	US-09-352-616A-114
13	100	100.0	241	4	US-09-232-149A-114
14	100	100.0	241	4	US-09-159-812-114
15	100	100.0	241	4	US-09-636-215-114
16	100	100.0	241	4	US-09-685-166A-114
17	100	100.0	241	4	US-09-115-433-114
18	100	100.0	241	4	US-09-688-489-114
19	100	100.0	241	4	US-09-679-426-114
20	100	100.0	241	4	US-09-759-143-114
21	100	100.0	241	4	US-09-651-236-114
22	47	47.0	93	4	US-09-543-681A-6787
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26	43	43.0	155	4	US-09-543-681A-7489
27	43	43.0	159	4	US-09-540-236-1985

28 43 43.0 777 4 US-09-917-254-57 Sequence 57, Appli
29 42 42.0 281 3 US-09-320-878-5 Sequence 5, Appli
30 42 42.0 281 3 US-09-105-537-43 Sequence 43, Appli
31 42 42.0 281 4 US-09-141-308-6 Sequence 6, Appli
32 42 42.0 281 4 US-09-657-440-5 Sequence 5, Appli
33 42 42.0 303 4 US-09-583-110-4065 Sequence 4065, Ap
34 42 42.0 309 4 US-09-107-433-3802 Sequence 3802, Ap
35 42 42.0 327 4 US-09-489-039A-13790 Sequence 13790, A
36 42 42.0 435 1 US-08-374-155A-5 Sequence 5, Appli
37 42 42.0 435 2 US-08-785-396-5 Sequence 5, Appli
38 42 42.0 600 1 US-08-374-155A-10 Sequence 10, Appli
39 42 42.0 600 2 US-08-785-396-10 Sequence 10, Appli
40 42 42.0 607 3 US-09-204-208A-11 Sequence 11, Appli
41 42 42.0 607 4 US-10-072-436-11 Sequence 11, Appli
42 42 42.0 629 1 US-08-374-155A-4 Sequence 4, Appli
43 42 42.0 629 2 US-08-785-396-4 Sequence 4, Appli
44 42 42.0 831 4 US-09-289-861A-8 Sequence 8, Appli
45 42 42.0 11877 3 US-09-105-537-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-439-313-522
; Sequence 522, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-439-313-522

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Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LLVVPALIKDYGSGEDFTQV 20
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Db 1 LLVVPALIKDYGSGEDFTQV 20

RESULT 2
US-09-636-215-522
; Sequence 522, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-636-215-522

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Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLVVPAAKDKYGSQEDFTQV 20

RESULT 3
US-09-685-166A-522
Sequence 522, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-685-166A-522

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Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 LLVVPAAKDKYGSQEDFTQV 20
RESULT 4
US-09-679-426-522
Sequence 522, Application US/09679426
Patent No. 6759515
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-679-426-522

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLVVPAAKDKYGSQEDFTQV 20

RESULT 5
US-09-759-143-522
Sequence 522, Application US/09759143
Patent No. 6800746
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRN
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-759-143-522

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Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLVWPAIKDYGSQSDFTQV 20

RESULT 6
US-09-651-236-522
Sequence 522, Application US/09651236
Patent No. 6818751
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRN
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-651-236-522

Query Match 100.0%; Score 100; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLVWPAIKDYGSQSDFTQV 20

RESULT 7
US-09-148-545-137
Sequence 137, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
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EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
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; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
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; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,909
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; EARLIER APPLICATION NUMBER: 60/056,875
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; EARLIER APPLICATION NUMBER: 60/056,862
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; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

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Db 111 LLVPAIKKDYGSQEDFTQV 130

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; Sequence 1, Application US/08808148
; Patent No. 6020478
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer

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1  RESULT 9
2  US-09-020-956-114
3  ; Sequence 114, Application US/09020956
4  ; Patent No. 6261562
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Xu, Jiangchun C.
7  ; APPLICANT: Dillin, Davin C.
8  ; TITLE OF INVENTION: COMPOUNDS FOR
9  ; NUMBER OF SEQUENCES: 178
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: SEED and BERRY LLP
12 ; STREET: 6300 Columbia Center, 7
13 ; CITY: Seattle
14 ; STATE: WA
15 ; COUNTRY: USA
16 ; ZIP: 98104
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ; OPERATING SYSTEM: PC-DOS/MS-DOS
21 ; SOFTWARE: Patent In Release #1.0
22 ; CURRENT APPLICATION DATA:

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US-09-030-607-114

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Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels

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; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121-42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-114

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Query Match      100.0%; Score 100; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 6e-10;
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Db 120 LLVVPAAKKDYGSQEDFTQV 139

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 20:00:18 ; Search time 74.9153 Seconds
(without alignments)
86.952 Million cell updates/sec

Title: us-09-780-669-114_COPY_120_139

Perfect score: 100

Sequence: 1 LLVVPALKYGSQEDFTQV 20

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Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	20	9	US-09-759-143-522
2	100	100.0	20	9	US-09-780-669-522
3	100	100.0	20	9	US-09-822-827-522
4	100	100.0	20	9	US-09-895-793-522
5	100	100.0	20	9	US-09-895-814-522
6	100	100.0	20	13	US-10-012-896-522
7	100	100.0	20	14	US-10-010-940-522
8	100	100.0	20	14	US-10-144-678A-522
9	100	100.0	20	14	US-10-294-025-522
10	100	100.0	126	11	US-09-978-360A-555
11	100	100.0	233	9	US-09-981-876-137
12	100	100.0	233	10	US-09-148-545-137
13	100	100.0	240	15	US-10-264-237-1489

14	100	100.0	241	9	US-09-759-143-114
15	100	100.0	241	9	US-09-780-669-114
16	100	100.0	241	9	US-09-030-606-114
17	100	100.0	241	9	US-09-822-827-114
18	100	100.0	241	9	US-09-115-453-114
19	100	100.0	241	9	US-09-232-880-114
20	100	100.0	241	9	US-09-908-193-44
21	100	100.0	241	9	US-09-895-793-114
22	100	100.0	241	9	US-09-895-814-114
23	100	100.0	241	13	US-10-012-896-114
24	100	100.0	241	14	US-10-097-340-326
25	100	100.0	241	14	US-10-010-940-114
26	100	100.0	241	14	US-10-205-823-425
27	100	100.0	241	14	US-10-144-678A-114
28	100	100.0	241	14	US-10-294-025-114
29	100	100.0	241	15	US-10-235-027-604
30	100	100.0	241	15	US-10-037-417-77
31	100	100.0	241	15	US-10-037-417-78
32	100	100.0	241	16	US-10-688-838-114
33	100	100.0	258	14	US-10-097-340-324
34	100	100.0	258	14	US-10-205-823-423
35	100	100.0	273	14	US-10-156-136-20
36	84	84.0	240	9	US-09-908-193-43
37	84	84.0	240	10	US-09-823-187-74
38	84	84.0	240	15	US-10-037-417-76
39	84	84.0	241	15	US-10-037-417-22
40	62	62.0	103	11	US-09-864-408A-3062
41	47	47.0	549	15	US-10-369-493-195
42	46	46.0	102	14	US-10-317-832-48
43	46	46.0	206	15	US-10-424-599-275188
44	45	45.0	89	15	US-10-282-122A-59382
45	45	45.0	103	11	US-09-864-408A-1342

ALIGNMENTS

RESULT 1

US-09-759-143-522
; Sequence 522, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 522
; LENGTH: 20
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-759-143-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSQEDFTQV 20
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Db 1 LLVVPAAKKDYGSQEDFTQV 20
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RESULT 2

US-09-780-669-522
; Sequence 522, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 522

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-780-669-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSQEDFTQV 20
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Db 1 LLVVPAAKKDYGSQEDFTQV 20
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RESULT 3

US-09-822-827-522
; Sequence 522, Application US/09822827

; Patent No. US20020091680A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C1

; CURRENT APPLICATION NUMBER: US/09/822,827

; CURRENT FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 522

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-822-827-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLVVPAAKKDYGSQEDFTQV 20
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RESULT 4

US-09-895-793-522

; Sequence 522, Application US/09895793

; Publication No. US20020192763A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William T.

; APPLICANT: Henderson, Robert A.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Vinals de Bassols, Carlota

; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C2

; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 522

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-895-793-522

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Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLVVPAAKKDYGSQEDFTQV 20
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Db 1 LLVVPAAKKDYGSQEDFTQV 20
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RESULT 5

US-09-895-814-522

; Sequence 522, Application US/09895814

; Publication No. US20020193296A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-895-814-522

Query Match 100.0%; Score 100; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLVVPAlKKDYGSQEDFTQV 20

RESULT 6
US-10-012-896-522
Sequence 522, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-10-012-896-522

Query Match 100.0%; Score 100; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 1 LLVVPAlKKDYGSQEDFTQV 20

RESULT 7
US-10-010-940-522
Sequence 522, Application US/10010940
Publication No. US20030088062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqiu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 522
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-10-010-940-522

Query Match 100.0%; Score 100; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPAlKKDYGSQEDFTQV 20
Db 1 LLVVPAlKKDYGSQEDFTQV 20

RESULT 8
US-10-144-678A-522
Sequence 522, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.

1	PRIOR FILING DATE: 1997-04-11	
2	PRIOR APPLICATION NUMBER: 60/043,312	
3	PRIOR FILING DATE: 1997-04-11	
4	PRIOR APPLICATION NUMBER: 60/043,313	
5	PRIOR FILING DATE: 1997-04-11	
6	PRIOR APPLICATION NUMBER: 60/043,313	
7	PRIOR FILING DATE: 1997-04-11	
8	PRIOR APPLICATION NUMBER: 60/043,672	
9	PRIOR FILING DATE: 1997-04-11	
10	PRIOR APPLICATION NUMBER: 60/043,315	
11	PRIOR FILING DATE: 1997-04-11	
12	PRIOR APPLICATION NUMBER: 60/048,974	
13	PRIOR FILING DATE: 1997-06-06	
14	PRIOR APPLICATION NUMBER: 60/056,886	
15	PRIOR FILING DATE: 1997-08-22	
16	PRIOR APPLICATION NUMBER: 60/056,877	
17	PRIOR FILING DATE: 1997-08-22	
18	PRIOR APPLICATION NUMBER: 60/056,889	
19	PRIOR FILING DATE: 1997-08-22	
20	PRIOR APPLICATION NUMBER: 60/056,893	
21	PRIOR FILING DATE: 1997-08-22	
22	PRIOR APPLICATION NUMBER: 60/056,630	
23	PRIOR FILING DATE: 1997-08-22	
24	PRIOR APPLICATION NUMBER: 60/056,878	
25	PRIOR FILING DATE: 1997-08-22	
26	PRIOR APPLICATION NUMBER: 60/056,662	
27	PRIOR FILING DATE: 1997-08-22	
28	PRIOR APPLICATION NUMBER: 60/056,872	
29	PRIOR FILING DATE: 1997-08-22	
30	PRIOR APPLICATION NUMBER: 60/056,882	
31	PRIOR FILING DATE: 1997-08-22	
32	PRIOR APPLICATION NUMBER: 60/056,637	
33	PRIOR FILING DATE: 1997-08-22	
34	PRIOR APPLICATION NUMBER: 60/056,903	
35	PRIOR FILING DATE: 1997-08-22	
36	PRIOR APPLICATION NUMBER: 60/056,888	
37	PRIOR FILING DATE: 1997-08-22	
38	PRIOR APPLICATION NUMBER: 60/056,879	
39	PRIOR FILING DATE: 1997-08-22	
40	PRIOR APPLICATION NUMBER: 60/056,880	
41	PRIOR FILING DATE: 1997-08-22	
42	PRIOR APPLICATION NUMBER: 60/056,894	
43	PRIOR FILING DATE: 1997-08-22	
44	PRIOR APPLICATION NUMBER: 60/056,911	
45	PRIOR FILING DATE: 1997-08-22	
46	PRIOR APPLICATION NUMBER: 60/056,636	
47	PRIOR FILING DATE: 1997-08-22	
48	PRIOR APPLICATION NUMBER: 60/056,874	
49	PRIOR FILING DATE: 1997-08-22	
50	PRIOR APPLICATION NUMBER: 60/056,910	
51	PRIOR FILING DATE: 1997-08-22	
52	PRIOR APPLICATION NUMBER: 60/056,864	
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54	PRIOR APPLICATION NUMBER: 60/056,631	
55	PRIOR FILING DATE: 1997-08-22	
56	PRIOR APPLICATION NUMBER: 60/056,845	
57	PRIOR FILING DATE: 1997-08-22	
58	PRIOR APPLICATION NUMBER: 60/056,892	
59	PRIOR FILING DATE: 1997-08-22	
60	PRIOR APPLICATION NUMBER: 60/047,595	
61	PRIOR FILING DATE: 1997-08-23	
62	PRIOR APPLICATION NUMBER: 60/057,761	
63	PRIOR FILING DATE: 05-Sep-1997	
64	PRIOR APPLICATION NUMBER: 60/047,599	
65	PRIOR FILING DATE: 1997-05-23	
66	PRIOR APPLICATION NUMBER: 60/047,588	
67	PRIOR FILING DATE: 1997-05-23	
68	PRIOR APPLICATION NUMBER: 60/047,585	
69	PRIOR FILING DATE: 1997-05-23	
70	PRIOR APPLICATION NUMBER: 60/047,586	
71	PRIOR FILING DATE: 1997-05-23	
72	PRIOR APPLICATION NUMBER: 60/047,590	
73	PRIOR FILING DATE: 1997-05-23	
74	PRIOR APPLICATION NUMBER: 60/047,594	
75	PRIOR FILING DATE: 1997-05-23	

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; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

Query Match      100.0%; Score 100; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LLVVPAlKKDYGSQEDFTQV 20
        |||||
Db      111 LLVVPAlKKDYGSQEDFTQV 130

RESULT 12
US-09-148-545-137
; Sequence 137, Application US/09148545
; Publication No. US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
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; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
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; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11

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, EARLIER FILING DATE: 1997-04-11
, EARLIER APPLICATION NUMBER: 60/043,576
, EARLIER FILING DATE: 1997-04-11
, EARLIER APPLICATION NUMBER: 60/047,501
, EARLIER FILING DATE: 1997-08-23
, EARLIER APPLICATION NUMBER: 60/043,670
, EARLIER FILING DATE: 1997-04-11
, EARLIER APPLICATION NUMBER: 60/056,632
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,664
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,876
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,881
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,909
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,875
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,862
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,887
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/056,908
, EARLIER FILING DATE: 1997-08-22
, EARLIER APPLICATION NUMBER: 60/048,964
, EARLIER FILING DATE: 1997-06-06
, EARLIER APPLICATION NUMBER: 60/057,650
, EARLIER FILING DATE: 1997-09-05
, EARLIER APPLICATION NUMBER: 60/056,884
, EARLIER FILING DATE: 1997-08-22
, NUMBER OF SEQ ID NOS: 280
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 137
, LENGTH: 233

Query Match          100.0%; Score 1
Best Local Similarity 100.0%; Pred. N
Matches 20; Conservative 0; Mismatch

QY 1 LLVVPAlKKDYGSGEDFTQV 20
    |||||
Db 111 LLVVPAlKKDYGSGEDFTQV 130

RESULT 13
US-10-264-237-1489
, Sequence 1489, Application US/10264237
, Publication No. US20040009491A1
, GENERAL INFORMATION:
, APPLICANT: Birse et al.
, TITLE OF INVENTION: Nucleic Acids, Proteins
, FILE REFERENCE: PA131P1
, CURRENT APPLICATION NUMBER: US/10/264,237
, CURRENT FILING DATE: 2002-10-04
, PRIOR APPLICATION NUMBER: PCT/US01/1645
, PRIOR FILING DATE: 2001-05-18
, PRIOR APPLICATION NUMBER: US 60/205,515
, PRIOR FILING DATE: 2000-05-19
, NUMBER OF SEQ ID NOS: 2876
, SOFTWARE: PatentIn Ver. 3.1
, SEQ ID NO 1489
, LENGTH: 240
, TYPE: PRT
, ORGANISM: Homo sapiens
US-10-264-237-1489

Query Match          100.0%; Score 1
Best Local Similarity 100.0%; Pred. N
Matches 20; Conservative 0; Mismatch

QY 1 LLVVPAlKKDYGSGEDFTQV 20
    |||||

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Db 119 LLVPAIKDYGSQEDFTQV 138

RESULT 14

US-09-759-143-114
; Sequence 114, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-114

Query Match 100.0%; Score 100; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVPAIKDYGSQEDFTQV 20
|||
Db 120 LLVPAIKDYGSQEDFTQV 139

RESULT 15

US-09-780-669-114
; Sequence 114, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-114
Query Match 100.0%; Score 100; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLVPAIKDYGSQEDFTQV 20
|||
Db 120 LLVPAIKDYGSQEDFTQV 139
Search completed: February 5, 2005, 20:11:30
Job time : 75.9153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:49:45 ; Search time 19.661 Seconds
(without alignments)
97.876 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139

Perfect score: 100

Sequence: 1 LLVVPALIKDYGSGEDFTQV 20

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	241	2 A59262	tetraspan TSPAN-1
2	49	49.0	347	2 AC2456	hypothetical prote
3	49	49.0	764	2 B82303	conserved hypotet
4	47	47.0	89	2 AG0002	conserved hypotet
5	47	47.0	172	2 C81726	conserved hypotet
6	46	46.0	303	2 AC1087	PTS system mannose
7	45	45.0	268	2 S17446	photosystem II oxy
8	45	45.0	521	2 D88640	protein F55A8.2 [i
9	45	45.0	1274	2 T37193	enamelin matrix pr
10	44.5	44.5	248	2 S03888	photosystem II oxy
11	44.5	44.5	260	2 S10016	photosystem II oxy
12	44.5	44.5	263	2 JC5271	oxygen-evolving co
13	44.5	44.5	267	2 S00005	photosystem II oxy
14	44	44.0	92	2 H82371	conserved hypotet
15	44	44.0	402	1 E70302	molybdenum cofacto
16	44	44.0	706	2 C71929	hypothetical prote
17	43.5	43.5	272	2 D95038	PTS system, IID co
18	43.5	43.5	272	2 G97908	hypothetical prote
19	43	43.0	88	2 A46411	conserved hypotet
20	43	43.0	89	2 C86073	hypothetical prote
21	43	43.0	89	2 C86073	hypothetical prote
22	43	43.0	89	2 S40804	hypothetical prote
23	43	43.0	144	2 S23661	superoxide dismuta
24	43	43.0	222	1 DSRTN	superoxide dismuta
25	43	43.0	222	2 I57023	superoxide dismuta
26	43	43.0	303	2 AB1451	PTS system mannose
27	43	43.0	545	2 A87136	hypothetical prote
28	43	43.0	1062	2 S46367	protein kinase CDC
29	42.5	42.5	258	2 S22763	photosystem II oxy

30 42 42.0 256 2 F89955 conserved hypotet
31 42 42.0 257 2 F86697 hypothetical prote
32 42 42.0 281 2 T17413 thioesterase II (E
33 42 42.0 303 2 C97904 phosphotransferase
34 42 42.0 303 2 C95033 PTS system, mannose
35 42 42.0 360 1 A46409 alcohol dehydrogen
36 42 42.0 562 2 C82263 trehalose-6-phosph
37 42 42.0 612 2 T39684 hypothetical prote
38 41.5 41.5 257 2 G84712 hypothetical prote
39 41.5 41.5 258 1 P2TOX2 photosystem II oxy
40 41.5 41.5 596 2 T04506 hypothetical prote
41 41 41.0 89 2 AD0951 conserved hypotet
42 42 41.0 209 2 B97797 superoxide dismuta
43 41 41.0 213 2 E64568 superoxide dismuta
44 41 41.0 223 2 S48832 superoxide dismuta
45 41 41.0 223 2 S48831 superoxide dismuta

ALIGNMENTS

RESULT 1

A59262

tetraspan TSPAN-1 - human

C:Species: Homo sapiens (man)

C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C:Accession: A59262

R:Todd, S.C.; Doctor, V.S.; Levy, S.

Biochim. Biophys. Acta 1399, 101-104, 1998

A:Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.

A:Reference number: A59258; MUID:98390278; PMID:9714763

A:Accession: A59262

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-241 <TOD>

A:Cross-references: UNIPROT:O60635; GB:AF054838; NID:G2997740; PIDN:AAC69714.1; PID:G299

C:Genetics:

A:Gene: TSPAN-1

C:Superfamily: CD9 antigen

Query Match 100.0%; Score 100; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLVVPALIKDYGSGEDFTQV 20
Db 120 LLVVPALIKDYGSGEDFTQV 139

RESULT 2

AC2456

hypothetical protein alr5203 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AC2456

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AC2456

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-347 <CUR>

A:Cross-references: UNIPROT:Q8YLU3; GB:BA000019; PIDN:BA076902.1; PID:G17134342; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr5203

Query Match 49.0%; Score 49; DB 2; Length 347;
Best Local Similarity 52.6%; Pred. No. 3.3;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

A;Accession: S17446
A;Molecule type: mRNA
A;Residues: 8-268 <HUA>
A;Cross-references: UNIPROT:P18212; UNIPROT:Q04125; UNIPROT:Q0458; UNIPROT:Q04125; UNIPROT:Q04125
A;Accession: S17445
A;Molecule type: DNA
A;Residues: 1-229 <HU2>

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Qy 3 VVPAIKK---DYGSQEDF-TQV 20
Db 145 VTPTDKSITDYGSPEEFLTV 166

RESULT 8
D88640
protein F55A8.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C:Accession: D88640
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: AY5000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88640
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-521 <STO>
A:Cross-references: GB:chr_IV; PIDN:AAC19186.1; PID:g3193148; GSPDB:GN00022; CESP:F55A8
C:Genetics:
A:Gene: F55A8.2
A:Map position: 4
C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-bi

Query Match 45.0%; Score 45; DB 2; Length 521;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 6 AIKIDYGSQEDFTQV 20
Db 154 SLKXDYGDKERLAQV 168

RESULT 9
T37193
enamelin matrix protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37193
R:Hu, C.C.; Slimer, J.P.; Bartlett, J.D.; Nanci, A.; Qian, Q.; Zhang, C.; Ryu, O.H.; Xue
submitted to the EMBL Data Library, December 1996
A:Description: Cloning and characterization of mouse enamel.
A:Reference number: Z21631
A:Accession: T37193
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1274 <HUC>
A:Cross-references: UNIPROT:O55196; EMBL:U82698; NID:g2737960; PID:g2737961; PIDN:AAB943
A:Experimental source: strain Swiss-Webster; enamel organ epithelia

Query Match 45.0%; Score 45; DB 2; Length 1274;
Best Local Similarity 42.9%; Pred. No. 59;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VVPAIKDYGSQED 16
Db 711 ILPLKEDYGRQDE 724

RESULT 10
S03888
Photosystem II oxygen-evolving complex protein 2 precursor - white mustard (fragment)
N:Alternate names: photosystem II extrinsic membrane protein 23K chain
C:Species: Sinapis alba (white mustard)
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S03888
R:Wenng, A.; Ehmann, B.; Schaefer, E.
FEBS Lett. 246, 140-144, 1989
A:Title: The 23 kDa polypeptide of the photosynthetic oxygen-evolving complex from mustard
undance.

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Job time : 20.661 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:36:20 ; Search time 94.9153 Seconds
(without alignments)
107.902 Million cell updates/sec

Title: US-09-780-669-114_COPY_120_139
Perfect score: 100
Sequence: 1 LLVPAIKKYGSOEDFTQV 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	241	1 TSNI_HUMAN	O60635 homo sapien
2	84	84.0	240	2 Q99J59	Q99J59 mus musculu
3	76	76.0	241	2 Q6AYR9	Q6AYR9 rattus norv
4	51	51.0	548	2 Q813H5	Q813H5 plasmodium
5	50.5	50.5	253	2 Q734B5	Q734B5 bacillus ce
6	49	49.0	347	2 Q8YLU3	Q8YLU3 anabaena sp
7	49	49.0	764	2 Q9KUB9	Q9KUB9 vibrio chol
8	48	48.0	173	2 Q9P919	Q9P919 pneumocysti
9	47	47.0	89	2 Q66GG7	Q66GG7 yersinia ps
10	47	47.0	89	2 Q9RB12	Q9RB12 pectobacter
11	47	47.0	89	2 Q8ZJS3	Q8ZJS3 yersinia pe
12	47	47.0	89	2 Q6DB80	Q6DB80 erwinia car
13	47	47.0	172	2 Q9PL73	Q9PL73 chlamydia m
14	46	46.0	74	2 Q8LTS5	Q8LTS5 lactococcus
15	46	46.0	74	2 Q77910	Q77910 lactococcus
16	46	46.0	74	2 Q9G0E7	Q9G0E7 lactococcus
17	46	46.0	107	2 Q6FD93	Q6FD93 acinetobact
18	46	46.0	303	2 Q7WYV1	Q7WYV1 streptococc
19	46	46.0	303	2 Q8YAM0	Q8YAM0 listeria mo
20	46	46.0	303	2 Q724V8	Q724V8 listeria mo
21	45.5	45.5	600	2 Q7VD65	Q7VD65 prochloroco
22	45	45.0	88	2 Q65QJ5	Q65QJ5 manheimia
23	45	45.0	101	1 RS24_METWA	Q6PZ95 methanosarc
24	45	45.0	222	2 Q6B7B8	Q6B7B8 spirometra
25	45	45.0	255	2 Q93H75	Q93H75 streptomyce
26	45	45.0	264	2 Q7VFH5	Q7VFH5 helicobacte
27	45	45.0	268	1 P8P1_TOBAC	Q7dm39 nicotiana t
28	45	45.0	268	2 Q40457	Q40457 nicotiana t
29	45	45.0	470	2 Q688A8	Q688A8 caenorhabdi
30	45	45.0	601	2 Q7PYT9	Q7PYT9 anopheles g
31	45	45.0	737	2 Q7KPJ2	Q7KPJ2 caenorhabdi

32	45	45.0	743	2 Q688A9	Q688A9 caenorhabdi
33	45	45.0	749	2 Q8MXG7	Q8MXG7 caenorhabdi
34	45	45.0	780	2 Q76360	Q76360 caenorhabdi
35	45	45.0	1274	1 ENAM_MOUSE	O5196 mus musculu
36	44.5	44.5	217	1 PSBP_BRAJU	Q6334 brassica ju
37	44.5	44.5	253	2 Q637Y5	Q637Y5 bacillus ce
38	44.5	44.5	260	1 PSBP_SINAL	P11594 sinapis alb
39	44.5	44.5	263	1 P8P1_ARATH	Q42029 arabidopsis
40	44.5	44.5	267	1 PSBP_SPTOL	P12302 spinacia ol
41	44.5	44.5	294	2 Q9BLK9	Q9BLK9 bombyx mori
42	44	44.0	92	2 Q9KVV2	Q9KVV2 vibrio chol
43	44	44.0	101	1 RS24_METAC	Q8jt2 methanosarc
44	44	44.0	166	2 Q6MBI9	Q6mbi9 parachlamyd
45	44	44.0	172	2 Q9P922	Q9p922 pneumocysti

ALIGNMENTS

RESULT 1
TSNI_HUMAN
ID TSNI_HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tetraspanin 1 (Tspan-1) (Tetraspanin NET-1) (Tetraspanin TM4-C).
GN Name=TSNPANI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TM4SF family";
RL Biochim. Biophys. Acta 1399:101-104 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database";
RN [3]
RP Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspanins";
RN [4]
RP Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; AF054838; AAC69714.1; -
 DR EMBL; AF065388; AAC17119.1; -
 DR EMBL; AF133425; AAF08364.1; -
 DR EMBL; BC007290; AAH07290.1; -
 DR EMBL; BC013404; AAH13404.1; -
 DR PIR; A59262; A59262.
 DR H-InvDB; HIX0000543; -
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR008952; Tetraspanin.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Tetraspanin; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4.1; FALSE_NEG.
 DR Glycoprotein; transmembrane.
 FT DOMAIN 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT DOMAIN 33 52 Extracellular (Potential).
 FT TRANSMEM 53 73 Potential.
 FT DOMAIN 74 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 109 Potential.
 FT DOMAIN 110 211 Extracellular (Potential).
 FT TRANSMEM 212 232 Potential.
 FT DOMAIN 233 241 Cytoplasmic (Potential).
 FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 189 189 K -> E (in Ref. 1).
 SQ SEQUENCE 241 AA; 26301 MW; AF938AD7147CB884 CRC64;
 Query Match 100.0%; Score 100; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LLVVPALKDYGSGEDPTQV 20
 DB 120 LLVVPALKDYGSGEDPTQV 139
 RESULT 2
 Q99059 PRELIMINARY; PRT; 240 AA.
 AC Q99J59;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE RIKEN cDNA 9030418M05 (Mus musculus adult male colon cDNA, RIKEN full-
 DE length enriched library, clone:9030418M05 product:similar to tetraspan
 DE TSPAN-1).
 DE Name=9030418M05Rik;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schmerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RA The RIKEN Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [7]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [8]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Kojima H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saigo H., Saigo R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toyota T., Yamamura T., Yamana K., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC003448; AAC03448.1; -;
DR EMBL; BC007869; AAC07869.1; -;
DR MGD; MGI:1914055; 9030418M05Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00342; RHESUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4.1; 1.
SQ SEQUENCE 240 AA; 26356 MW; AD4C448A32BC2999 CRC64;

Query Match 84.0%; Score 84; DB 2; Length 240;
Best Local Similarity 85.0%; Pred. No. 7.9e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LLVPAIKKDYGSQEDFTQV 20
|||||:||||:||||:
Db 120 LLVPAIEKDYGYQTEFTQV 139

RESULT 3

Q6AYR9 PRELIMINARY; PRT; 241 AA.
AC Q6AYR9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tetraspan 1.
GN Name=MGC93753;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Tringali J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC078938; AAH78938.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00342; RHESUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4.1; 1.
SQ SEQUENCE 241 AA; 26453 MW; 9118B865464D1A70 CRC64;

Query Match 76.0%; Score 76; DB 2; Length 241;
Best Local Similarity 78.9%; Pred. No. 0.00019;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LLVPAIKKDYGSQEDFTQV 20
|||||:||||:||||:
Db 121 LLVPAIEKDYGYQTEFTQV 139

RESULT 4

Q8I3H5 PRELIMINARY; PRT; 548 AA.
AC Q8I3H5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sugar transporter, putative.
GN Name=PF01455w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Devin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sultston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531 (2002)
DR EMBL; AL929354; CA051553.1; -;
SQ SEQUENCE 548 AA; 63768 MW; 245CACDS95067CF3 CRC64;

Query Match 51.0%; Score 51; DB 2; Length 548;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LLVPAIKKDYGSQEDFTQV 20
|||||:||||:||||:
Db . 264 ITVLVINKDYKSKEDFVQL 283

RESULT 5

Q734B5 PRELIMINARY; PRT; 253 AA.
ID Q734B5
AC Q734B5;

```
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CAX amino terminal protease family.
GN OrderedLocusNames=BCE3492;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=22523;
RN [1]
SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.1";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017275; AAS42398.1; -.
DR TIGR; BCE3492; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi; 1.
KW Complete proteome; Protease.
SQ SEQUENCE 253 AA; 28985 MW; 9572AA6F36352785 CRC64;

Query Match 50.5%; Score 50.5; DB 2; Length 253;
Best Local Similarity 55.0%; Pred. No. 4.7;
Matches 11; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

QY 3 VVPAI-----KKDYGSGEDF 17
   :|||  |||  |||  |||  |||
Db 48 IMPAIIAISLKKYGSQEEF 67

RESULT 6
ID Q8YLU3 PRELIMINARY; PRT; 347 AA.
AC Q8YLU3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alr5203 protein.
GN OrderedLocusNames=alr5203;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC NCBI_TaxID=103690;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003599; BAB76902.1; -.
DR PIR; AC2456; AC2456.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 347 AA; 40541 MW; AFBC249221FEB26D CRC64;

Query Match 49.0%; Score 49; DB 2; Length 347;
Best Local Similarity 52.6%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LVVPAIKKDYGSQEDFTQV 20
   |.|  |||  |||  |||  |||
Db 329 LEUPIIKKEISSVKEFTQV 347

RESULT 7
ID Q9KUB9 PRELIMINARY; PRT; 764 AA.
AC Q9KUB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VC0603.
GN OrderedLocusNames=VC0603;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=666;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406933; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004145; AAF93770.1; -.
DR PIR; B82303; B82303.
DR TIGR; VC0603; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 764 AA; 85616 MW; 0C3CC8BCA100C840 CRC64;

Query Match 49.0%; Score 49; DB 2; Length 764;
Best Local Similarity 45.0%; Pred. No. 29;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 LLVVPAPKDKYGSQEDFTQV 20
   :|||  |||  |||  |||  |||
Db 235 IIIAVDISTDYKSQEDFTNL 254

RESULT 8
ID Q9P919 PRELIMINARY; PRT; 173 AA.
AC Q9P919;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Manganese-dependent superoxide dismutase (EC 1.15.1.1)
DE (Fragment).
DE Name=soda;
GN Pneumocystis carinii f. sp. suis.
OS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OC NCBI_TaxID=112251;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20427437; PubMed=10975697;
RA Denis C.M., Mazars E., Guyot K., Odberg-Ferragut C., Viscogliosi E.,
RA Dei-Cas E., Wakefield A.B.;
RT "Genetic divergence at the SODA locus of six different formae
RT speciales of Pneumocystis carinii.";
RL Med. Mycol. 38:289-300(2000).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
```

CC family.
 DR EMBL; AF146755; AAF25727.1; -.
 DR HSSP; Q92450; 1KKC.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
 DR GO; GO:0006801; P:superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF02777; Sod_Fe_C; 1.
 DR Pfam; PF00081; Sod_Fe_N; 1.
 DR PRINTS; PR01703; MNSODISMTASE.
 DR PRODOM; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 DR Oxidoreductase.
 KW NON_TER 1
 FT NON_TER 173
 FT NON_TER 173
 SQ SEQUENCE 173 AA; 20099 MW; 691108FDD0005665B CRC64;
 Query Match 48.0%; Score 48; DB 2; Length 173;
 Best Local Similarity 50.0%; Pred. No. 8.3;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 3 VVPAIKKDYGSQEDFTQV 20
 DB 85 LVFAIKKEWGSVENFISI 102
 RESULT 9
 Q66GG7 PRELIMINARY; PRT; 89 AA.
 ID Q66GG7
 AC Q66GG7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=IPTB0015;
 OS Yersinia pseudotuberculosis IP 32953.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=273123;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IP 32953;
 RX PubMed=15358858;
 RA Chain P.S.G.; Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
 RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
 RA Simonet M., Chenail-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser L.J., Garcia E.;
 RT "Insights into the genome evolution of Yersinia pseudotuberculosis";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 DR EMBL; BX936398; CAH19255.1; -.
 DR InterPro; IPR009383; DUF1040.
 DR Pfam; PF06288; DUF1040; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 89 AA; 10168 MW; C240C03A620D66F9 CRC64;
 Query Match 47.0%; Score 47; DB 2; Length 89;
 Best Local Similarity 60.0%; Pred. No. 5.8;
 Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1;
 QY 3 VVPAIKKDYGSQEDF 17
 DB 64 VVPLKKDY--EEDF 76
 RESULT 10
 Q9RB12 PRELIMINARY; PRT; 89 AA.
 ID Q9RB12
 AC Q9RB12;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE YihD.
 GN Name=yihD;
 OS Pectobacterium carotovorum (subsp. carotovorum) (Erwinia carotovora
 (subsp. carotovora)).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCR1193;
 RX MEDLINE=99392457; PubMed=10463161;
 RA Vincent-Sealy L.V., Thomas J.D., Commander P., Salmoud G.P.;
 RT "Erwinia carotovora DsbA mutants: evidence for a periplasmic-stress
 signal transduction system affecting transcription of genes encoding
 secreted proteins";
 RL Microbiology 145:1945-1958(1999).
 DR EMBL; AF146615; AAD47615.1; -.
 DR InterPro; IPR009383; DUF1040.
 DR Pfam; PF06288; DUF1040; 1.
 SQ SEQUENCE 89 AA; 10402 MW; 228FDDDD71E865481 CRC64;
 Query Match 47.0%; Score 47; DB 2; Length 89;
 Best Local Similarity 60.0%; Pred. No. 5.8;
 Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1;
 QY 3 VVPAIKKDYGSQEDF 17
 DB 64 VVPLKKDY--EEDF 76
 RESULT 11
 Q8ZJS3 PRELIMINARY; PRT; 89 AA.
 ID Q8ZJS3
 AC Q8ZJS3; Q74YD0; Q7CG24;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein YPO0013a (Hypothetical protein y3814).
 GN Name=YPO0013a; OrderedLocusNames=YPO015, y3814;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague";
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM";
 RL J. Bacteriol. 184:4601-4611(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=91001 / Biovar Mediaevalis;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RL Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ414141; CAC88881.1; -;
 DR EMBL: AE013984; AAM87359.1; -;
 DR EMBL: AE017127; AAS60296.1; -;
 DR PIR: AG0002; AG0002;
 DR Pfam: PF06288; DUF1040; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 89 AA; 10168 MW; C240C03A620D66F9 CRC64;
 Query Match 47.0%; Score 47; DB 2; Length 89;
 Best Local Similarity 60.0%; Pred. No. 5.8;
 Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1;
 QY 3 VVPAIKKDYGSQEDF 17
 Db 64 VVPAIKKDYGSQEDF 76
 RESULT 12
 Q6DB80 PRELIMINARY; PRT; 89 AA.
 ID Q6DB80
 AC Q6DB80;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=ECA0018;
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=29471;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holve M.C., Thomson N.R., Bentley S.D., Church L.J.C., Mungall K.,
 RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.; Erwinia
 RT "Genome sequence of the enterobacterial phytopathogen of virulence
 RT carotovora subsp. atroseptica and characterization of virulence
 RT factors."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
 DR EMBL: BX950851; CAG72942.1; -;
 DR InterPro: IPR009383; DUF1040.
 DR Pfam: PF06288; DUF1040; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 89 AA; 10418 MW; 0CEFFDD71B8647A0 CRC64;
 Query Match 47.0%; Score 47; DB 2; Length 89;
 Best Local Similarity 60.0%; Pred. No. 5.8;
 Matches 9; Conservative 3; Mismatches 1; Indels 2; Gaps 1;
 QY 3 VVPAIKKDYGSQEDF 17
 Db 64 VVPAIKKDYGSQEDF 76
 RESULT 13
 Q9PL73 PRELIMINARY; PRT; 172 AA.
 ID Q9PL73
 AC Q9PL73;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein TC0235.
 GN OrderedLocusNames=TC0235;
 OS Chlamydia muridarum.
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83560;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=MoPn / Ni99;
 MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
 Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
 Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
 McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
 "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 pneumoniae A39."
 Nucleic Acids Res. 28:1397-1406(2000).
 EMBL: AF002290; AAF39106.1; -;
 PIR: C81726; C81726.
 TIGR: TC0235; -;
 InterPro: IPR007966; DUF720.
 Pfam: PF05302; DUF720; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 172 AA; 18923 MW; B56AA6C64AA88AAB CRC64;
 Query Match 47.0%; Score 47; DB 2; Length 172;
 Best Local Similarity 44.4%; Pred. No. 12;
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LLVPAIKKDYGSQEDFT 18
 Db 79 LLVPSLEKKGSDDEYT 96
 RESULT 14
 Q8LTS5 PRELIMINARY; PRT; 74 AA.
 ID Q8LTS5
 AC Q8LTS5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative cro-like repressor.
 OS Lactococcus lactis bacteriophage ul36.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=114416;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22066040; PubMed=12069529; DOI=10.1006/viro.2002.1401;
 RA Labrie S., Moineau S.;
 RT "Complete genomic sequence of bacteriophage ul36: demonstration of
 RT phage heterogeneity within the P335 quasi-species of lactococcal
 RT phages."
 RL Virology 296:308-320(2002).
 DR EMBL: AF349457; AAM75754.1; -;
 DR InterPro: IPR008003; DUF739.
 DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam: PF05339; DUF739; 1.
 SQ SEQUENCE 74 AA; 8559 MW; B42AF1806FAB767 CRC64;
 Query Match 46.0%; Score 46; DB 2; Length 74;
 Best Local Similarity 61.5%; Pred. No. 7.1;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 7 IKKDYGSQEDFTQ 19
 Db 12 IKKDYGSQEDFTQ 24
 RESULT 15
 Q77910 PRELIMINARY; PRT; 74 AA.
 ID Q77910
 AC Q77910;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative cro repressor.

GN Name=cro;
 OS Lactococcus bacteriophage phi31.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=46654;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21141825; PubMed=11229902;
 RX DOI=10.1128/AEM.67.3.1128-1139.2001;
 RA Madsen S.M., Mills D., Djordjevic G., Israelsen H., Klaenhammer T.R.;
 RT "Analysis of the genetic switch and replication region of a P335-type
 bacteriophage with an obligate lytic lifestyle on Lactococcus
 lactis.";
 RL Appl. Environ. Microbiol. 67:1128-1139(2001).
 DR EMBL; AJ292531; CAC04155.1; -
 DR InterPro; IPR008003; DUF739.
 DR InterPro; IPR010982; Lambda_like_DNA.
 DR Pfam; PF05339; DUF739; 1.
 SQ SEQUENCE 74 AA; 8533 MW; B42A2F18180B5867 CRC64;

Query Match 46.0%; Score 46; DB 2; Length 74;
 Best Local Similarity 61.5%; Pred. No. 7.1;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 IKKYGSGEDFTQ 19
 ||:|||||:
 Db 12 IKKYGSGQDFAK 24

Search completed: February 5, 2005, 20:04:40
 Job time : 97.9153 secs

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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:34:18 ; Search time 99.5085 Seconds
(without alignments)
73.847 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169
Perfect score: 106
Sequence: 1 GFTNYTDFEDSPYFKENSA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	19	4 AAM01157	AAM01157 Human pro
2	106	100.0	19	4 AAU69802	AAU69802 Human pro
3	106	100.0	19	4 AAG99042	AAG99042 Human pro
4	106	100.0	19	4 ABU71693	ABU71693 Prostate
5	106	100.0	19	5 ABB95262	ABB95262 Epitope m
6	106	100.0	19	6 ABR54374	ABR54374 Prostate
7	106	100.0	19	7 ADB13954	ADB13954 Human pro
8	106	100.0	19	7 ADG26370	ADG26370 Human pro
9	106	100.0	172	7 ADD69590	ADD69590 Human REM
10	106	100.0	174	8 ADP81123	ADP81123 Protein o
11	106	100.0	214	8 ADR65994	ADR65994 Human pro
12	106	100.0	214	8 ADR66892	ADR66892 Human pro
13	106	100.0	233	6 AAU75060	AAU75060 Human sec
14	106	100.0	233	6 ABO01936	ABO01936 Novel hum
15	106	100.0	240	4 AAG62153	AAG62153 Human P50
16	106	100.0	240	5 ABB89113	ABB89113 Human pol
17	106	100.0	241	2 AAU69386	AAU69386 Prostate
18	106	100.0	241	2 AAU59954	AAU59954 Amino aci
19	106	100.0	241	2 AAU71870	AAU71870 Human pro
20	106	100.0	241	2 AAW58380	AAW58380 Human sec
21	106	100.0	241	3 AAY82003	AAY82003 Human imm
22	106	100.0	241	3 AAG94412	AAG94412 Human pro
23	106	100.0	241	3 AAM01118	AAM01118 Human pro
24	106	100.0	241	4 AAU69764	AAU69764 Human pro
25	106	100.0	241	4 AAB74801	AAB74801 Prostate

ALIGNMENTS

RESULT 1

AAM01157
ID AAM01157 standard; peptide; 19 AA.

XX AAM01157;

DT 04-OCT-2001 (first entry)

XX Human prostate-specific peptide used in epitope mapping studies #14.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis.

XX Homo sapiens.

XX WO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
monitoring and treating prostate cancer in a patient and for use in
vaccines.

XX Claim 2; Page 399; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
prostate-specific proteins (II). (I) and (II) have cytostatic activity,
and can be used in vaccine production and gene therapy. (I), (II),
antibodies to (II), fusion proteins comprising (II), and isolated T cells
prepared using (I) or (II) are used to treat cancer in a patient. (I) and
the antibodies are also used in the detection of cancer in a patient. The
cancer that is diagnosed or treated is particularly prostate cancer. (I)
and (II) can be used in vaccines. The antibodies or (I) can be used for
monitoring the progression of cancer in a patient. (I) and (II) can also
be used to improve diagnostic and therapeutic methods for prostate
cancer. They can indicate the level of metastasis as well as the prostate

CC volume. AAH93357 to AAH93944 and AA01115 to AA01118 represent
 CC polynucleotide and amino acid sequences used in the exemplification of
 CC the present invention

CC SQ Sequence 19 AA;
 Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
 |||||
 Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 2
 AAU69802
 ID AAU69802 standard; peptide; 19 AA.
 XX AC AAU69802;
 XX DT 30-JAN-2002 (first entry)
 XX DE Human prostate protein epitope mapping peptide #1.
 XX DE Human; prostate cancer; ss; cytostatic; immunostimulant; tumour; antigen;
 XX DE epitope.
 XX OS Homo sapiens.
 XX PN WO200173032-A2.
 XX PD 04-OCT-2001.
 XX PF 27-MAR-2001; 2001WO-US009919.
 XX PR 27-MAR-2000; 2000US-00536857.
 XX PR 09-MAY-2000; 2000US-00568100.
 XX PR 12-MAY-2000; 2000US-00570737.
 XX PR 13-JUN-2000; 2000US-00593793.
 XX PR 27-JUN-2000; 2000US-00605783.
 XX PR 09-AUG-2000; 2000US-00636215.
 XX PR 29-AUG-2000; 2000US-00651236.
 XX PR 06-SEP-2000; 2000US-00657279.
 XX PR 02-OCT-2000; 2000US-00679426.
 XX PR 10-OCT-2000; 2000US-00685166.
 XX PR 09-NOV-2000; 2000US-00709729.
 XX PA (CORI-) CORIXA CORP.
 XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX WPI; 2001-639232/73.
 XX New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer.
 XX Claim 2; Page 400; 579pp; English.
 CC The invention relates to isolated prostate-specific polynucleotides,
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised
 CC against the polypeptides (or antigenic epitopes derived from them) and
 CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific peptide of the invention. The peptides either represent

CC antigenic epitopes or domains of prostate specific proteins

XX SQ Sequence 19 AA;
 Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
 |||||
 Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 3
 AAG99042
 ID AAG99042 standard; peptide; 19 AA.
 XX AC AAG99042;
 XX DT 25-SEP-2001 (first entry)
 XX DE Human prostate-specific epitope mapping peptide #14.
 XX DE Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
 XX DE chromosome 22q11.2; prostate-specific protein; chromosome 1;
 XX DE prostate specific antigen; PSA.
 XX OS Homo sapiens.
 XX PN WO200134802-A2.
 XX PD 17-MAY-2001.
 XX PF 09-NOV-2000; 2000WO-US030904.
 XX PR 12-NOV-1999; 99US-00439313.
 XX PR 18-NOV-1999; 99US-00443686.
 XX PA (CORI-) CORIXA CORP.
 XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
 XX WPI; 2001-308785/32.
 XX Isolated polypeptide comprising at least an immunogenic portion of a
 PT prostate-specific protein, useful in the diagnosis and therapy of
 PT prostate cancer.
 XX Claim 3; Page 299; 325pp; English.
 CC The present invention describes an isolated polypeptide (P1) comprising
 CC at least an immunogenic portion of a prostate-specific protein, or its
 CC variant. Also described are polynucleotides (N1) encoding (P1) and
 CC (N1) have cytostatic activity and can be used in vaccine production. The
 CC polypeptides, nucleic acids and antibodies from the present invention are
 CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
 CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
 CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
 CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
 CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
 CC and polypeptide sequences used in the exemplification of the present
 CC invention

XX SQ Sequence 19 AA;
 Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
 |||||
 Db 1 GFTNYTDFEDSPYFKENSA 19

CC prostate cancer therapy associated peptide. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docID=US20020192763

XX SQ Sequence 19 AA;
 Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFSDSPYKNSA 19
 Db 1 GFTNYTDFSDSPYKNSA 19

RESULT 5

ABB95262
 ID ABB95262 standard; peptide; 19 AA.

XX AC ABB95262;
 XX DT 19-JUL-2002 (first entry)

XX DE Epitope mapping study peptide SEQ ID NO 504.
 XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
 XX KW gene therapy.

XX OS Unidentified.
 XX FN US2002022248-A1.

XX PD 21-FEB-2002.

XX PF 12-JAN-2001; 2001US-00759143.

XX PR 25-FEB-1997; 97US-00806099.

XX PR 01-AUG-1997; 97US-00904804.

XX PR 10-FEB-1998; 98US-00020956.

XX PR 25-FEB-1998; 98US-00030607.

XX PR 14-JUL-1998; 98US-00115453.

XX PR 23-SEP-1998; 98US-00159812.

XX PR 15-JAN-1999; 99US-00232149.

XX PR 09-APR-1999; 99US-00288946.

XX PR 13-JUL-1999; 99US-00352616.

XX PR 12-NOV-1999; 99US-00439313.

XX PR 18-NOV-1999; 99US-00443686.

XX PR 14-JAN-2000; 2000US-00483672.

XX PR 27-MAR-2000; 2000US-00536857.

XX PR 09-MAY-2000; 2000US-00568100.

XX PR 12-MAY-2000; 2000US-00570737.

XX PR 13-JUN-2000; 2000US-00593793.

XX PR 27-JUN-2000; 2000US-00605783.

XX PR 10-AUG-2000; 2000US-00636215.

XX PR 29-AUG-2000; 2000US-00651236.

XX PR 06-SEP-2000; 2000US-00657279.

XX PR 02-OCT-2000; 2000US-00679426.

XX PR 10-OCT-2000; 2000US-00685166.

XX PA (XUJJ/) XU J.

XX PA (DILL/) DILLON D C.

XX PA (MITC/) MITCHAM J L.

XX PA (HARL/) HARLOCKER S L.

XX PA (JIAN/) JIANG Y.

XX PA (KALO/) KALOS M D.

XX PA (FANG/) FANGER G R.

XX PA (RETT/) RETTER M W.

XX PA (STOL/) STOLK J A.

XX PA (DAYC/) DAY C H.

XX PA (VEDV/) VEDVICK T S.

XX PA (CART/) CARTER D.

XX PA (LISX/) LI S X.

RESULT 4

ABU71693

ID ABU71693 standard; peptide; 19 AA.

XX AC ABU71693;
 XX DT 10-JUN-2003 (first entry)

XX DE Prostate cancer therapy associated peptide #15.
 XX KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA.

XX OS Homo sapiens.

XX FN US2002192763-A1.

XX PD 19-DEC-2002.

XX PF 29-JUN-2001; 2001US-00895793.

XX PR 04-OCT-1999; 99US-0157455P.

XX PR 04-OCT-2000; 2000US-00679272.

XX PR 28-MAR-2001; 2001US-00822827.

XX PA (XUJJ/) XU J.

XX PA (DILL/) DILLON D C.

XX PA (MITC/) MITCHAM J L.

XX PA (HARL/) HARLOCKER S L.

XX PA (JIAN/) JIANG Y.

XX PA (KALO/) KALOS M D.

XX PA (FANG/) FANGER G R.

XX PA (RETT/) RETTER M W.

XX PA (STOL/) STOLK J A.

XX PA (DAYC/) DAY C H.

XX PA (VEDV/) VEDVICK T S.

XX PA (CART/) CARTER D.

XX PA (LISX/) LI S X.

XX PA (WANG/) WANG A.

XX PA (SKEI/) SKEIKY Y A W.

XX PA (HEPL/) HEPLER W T.

XX PA (HEND/) HENDERSON R A.

XX PA (HURA/) HURAL J.

XX PA (MCNE/) MCNEILL P D.

XX PA (HOUG/) HOUGHTON R L.

XX PA (DBAS/) Y DE BASSOLS C V.

XX PA (FOYT/) FOY T M.

XX PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;

PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;

XX WPI; 2001-245062/25.

XX PT Prostate specific protein and its encoding polynucleotide, useful for the

PT treatment and diagnosis of prostate cancer.

XX PS Example 18; SEQ ID NO 504; 85pp; English.

XX CC The invention describes a fusion protein comprising at least one amino

CC acid sequence of immunogenic portions of any of the 3 sequences not

CC defined in the specification, or sequences having at least 70 or 90 %

CC sequence identity to any one of the 35 sequences defined in the USPTO web

CC site, which is encoded by any of the 4 nucleotide sequences not defined

CC in the specification. The fusion protein, composition and methods are

CC useful for diagnosing, preventing and/or treating cancer, particularly

CC prostate cancer. The proteins are useful as markers to indicate the

CC presence or absence of cancer. This is the amino acid sequence of a

PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 504; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC peptide described in the invention
XX
XX Sequence 19 AA;
SQ
Query Match 100.0%; Score 106; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19
RESULT 6
ABR54374
ID ABR54374 standard; protein; 19 AA.
XX
AC ABR54374;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific related peptide for epitope mapping SEQ ID 504.
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
XX immune response; prostate cancer.
XX
XX Homo sapiens.
XX
XX WO200289747-A2.
XX
XX 14-NOV-2002.
XX
XX 09-MAY-2002; 2002WO-US014753.
XX
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-008595814.
XX 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
XX McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
XX Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX

PS Example 18; Page 466; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX Sequence 19 AA;
SQ
Query Match 100.0%; Score 106; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19
RESULT 7
ADB13954
ID ADB13954 standard; peptide; 19 AA.
XX
AC ADB13954;
XX
DT 18-DEC-2003 (first entry)
XX
XX Human prostate protein P503S epitope mapping peptide #2101.
XX
XX Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
XX cell therapy; vaccine; T-cell epitope;
XX class I major histocompatibility complex allele; MHC; prostate cancer;
XX tumour; antigen presenting cell; epitope.
XX
XX Homo sapiens.
XX
XX US2003185830-A1.
XX
XX 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 23-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00433913.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-008595814.
XX 10-DEC-2001; 2001US-00012896.
XX 09-MAY-2002; 2002US-00144678.
XX

PA (CORI-) CORIXA CORP.
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
XX Example 18; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
CC peptides comprise a fragment ADBI3563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI358, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is an epitope or
CC peptide derived from one of the prostate specific proteins of the
CC invention. Note: Except where otherwise indicated, the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030185830.
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 106; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19
|||||
RESULT 8
ADG26370
ID ADG26370 standard; peptide; 19 AA.
XX
AC ADG26370;
XX
XX 26-FEB-2004 (first entry)
DT
XX Human prostate-specific polypeptide #43.
XX
XX Human; prostate-specific polypeptide; prostate cancer; cytostatic.
XX
XX Homo sapiens.

XX US2003157089-A1.
XX
XX 21-AUG-2003.
XX
XX 09-MAY-2002; 2002US-00144678.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 09-MAY-2001; 2001US-00852911.
XX 29-JUN-2001; 2001US-00895814.
XX 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
XX Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
XX Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
XX McNeill PD, Houghton RL, Vinals Y De BassolaC, Foy TW, Watanabe Y;
XX Mesgher MJ, Deng T;
XX WPI; 2003-777973/73.
XX
XX New polynucleotides encoding prostate specific polypeptides isolated from
XX a human prostate tumor cDNA library are useful to diagnose and treat
XX cancer particularly prostate cancer.
XX
XX Example 18; SEQ ID NO 504; 99pp; English.
XX
XX The invention relates to human prostate-specific polypeptides and the
XX polynucleotides encoding them. The invention also relates to an isolated
XX antibody or its antigen-binding fragment that specifically binds a
XX polypeptide of the invention, a method of detecting cancer in a patient
XX comprising contacting a biological sample of the patient with an agent
XX that binds a prostate-specific polypeptide and comparing the amount of
XX bound polypeptide compared to a predetermined cut-off value and a fusion
XX protein comprising a prostate-specific polypeptide. The sequences of the
XX invention are used to diagnose and treat cancer, particularly prostate
XX cancer. This sequence represents a human prostate-specific polypeptide of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification but was obtained in electronic format
XX directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 106; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFTNYTDFEDSPYFKENSA 19

Db	1 GFTNYTDFEDSPYFKENSA 19	1 GFTNYTDFEDSPYFKENSA 19	1 GFTNYTDFEDSPYFKENSA 19
Db	82 GFTNYTDFEDSPYFKENSA 100	82 GFTNYTDFEDSPYFKENSA 100	82 GFTNYTDFEDSPYFKENSA 100
RESULT 9			
ADD69590	ADD69590 standard; protein, 172 AA.	ADD69590 standard; protein, 172 AA.	ADD69590 standard; protein, 172 AA.
XX	ADD69590;	ADD69590;	ADD69590;
XX	15-JAN-2004 (first entry)	15-JAN-2004 (first entry)	15-JAN-2004 (first entry)
XX	Human REMAP protein - SEQ ID 19.	Human REMAP protein - SEQ ID 19.	Human REMAP protein - SEQ ID 19.
XX	human; receptor and membrane-associated protein; REMAP; cytosolic; antiarteriosclerotic; anticonvulsant; neuroprotective; neurotrophic; neuroprotective; anti-HIV; anti-allergic; anti-inflammatory; cerbroprotective; cell proliferative; cancer; atherosclerosis; neurological; thymolametic; cell proliferative; cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS; allergy; developmental; hypothyroidism; Cushing's syndrome; infection.	human; receptor and membrane-associated protein; REMAP; cytosolic; antiarteriosclerotic; anticonvulsant; neuroprotective; neurotrophic; neuroprotective; anti-HIV; anti-allergic; anti-inflammatory; cerbroprotective; cell proliferative; cancer; atherosclerosis; neurological; thymolametic; cell proliferative; cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS; allergy; developmental; hypothyroidism; Cushing's syndrome; infection.	human; receptor and membrane-associated protein; REMAP; cytosolic; antiarteriosclerotic; anticonvulsant; neuroprotective; neurotrophic; neuroprotective; anti-HIV; anti-allergic; anti-inflammatory; cerbroprotective; cell proliferative; cancer; atherosclerosis; neurological; thymolametic; cell proliferative; cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS; allergy; developmental; hypothyroidism; Cushing's syndrome; infection.
XX	Homo sapiens.	Homo sapiens.	Homo sapiens.
OS	WO2003048305-A2.	WO2003048305-A2.	WO2003048305-A2.
XX	12-JUN-2003.	12-JUN-2003.	12-JUN-2003.
XX	13-NOV-2002; 2002WO-US036759.	13-NOV-2002; 2002WO-US036759.	13-NOV-2002; 2002WO-US036759.
XX	13-NOV-2001; 2001US-0333097P.	13-NOV-2001; 2001US-0333097P.	13-NOV-2001; 2001US-0333097P.
XX	15-NOV-2001; 2001US-0335274P.	15-NOV-2001; 2001US-0335274P.	15-NOV-2001; 2001US-0335274P.
XX	14-DEC-2001; 2001US-0340542P.	14-DEC-2001; 2001US-0340542P.	14-DEC-2001; 2001US-0340542P.
XX	18-DEC-2001; 2001US-0342166P.	18-DEC-2001; 2001US-0342166P.	18-DEC-2001; 2001US-0342166P.
XX	11-JAN-2002; 2002US-0347580P.	11-JAN-2002; 2002US-0347580P.	11-JAN-2002; 2002US-0347580P.
XX	14-JAN-2002; 2002US-0348687P.	14-JAN-2002; 2002US-0348687P.	14-JAN-2002; 2002US-0348687P.
XX	(INCY-) INCYTE GENOMICS INC.	(INCY-) INCYTE GENOMICS INC.	(INCY-) INCYTE GENOMICS INC.
XX	Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y; Chavla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM; Thangavelu K, Lee S, Emerling BM, Kable AE, Khare R, Baughn MR; Gandhi AR, Iran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ; Lee EA, Swarnakar A, Kallick DA, Griffin JA, Elliott VS, Gorvad AE; Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U; Burrill JD, Blake JU, Ho A, Zheng W, Gao J;	Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y; Chavla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM; Thangavelu K, Lee S, Emerling BM, Kable AE, Khare R, Baughn MR; Gandhi AR, Iran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ; Lee EA, Swarnakar A, Kallick DA, Griffin JA, Elliott VS, Gorvad AE; Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U; Burrill JD, Blake JU, Ho A, Zheng W, Gao J;	Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y; Chavla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM; Thangavelu K, Lee S, Emerling BM, Kable AE, Khare R, Baughn MR; Gandhi AR, Iran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ; Lee EA, Swarnakar A, Kallick DA, Griffin JA, Elliott VS, Gorvad AE; Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U; Burrill JD, Blake JU, Ho A, Zheng W, Gao J;
XX	WPI: 2003-513744/48.	WPI: 2003-513744/48.	WPI: 2003-513744/48.
XX	N-PSDB; ADD69637.	N-PSDB; ADD69637.	N-PSDB; ADD69637.
XX	New human receptors and membrane-associated proteins (REMAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or infections.	New human receptors and membrane-associated proteins (REMAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or infections.	New human receptors and membrane-associated proteins (REMAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or infections.
XX	Claim 1; SEQ ID NO 19; 298pp; English.	Claim 1; SEQ ID NO 19; 298pp; English.	Claim 1; SEQ ID NO 19; 298pp; English.
XX	The invention relates to a novel isolated polypeptide comprising a human receptor and membrane-associated protein (REMAP). The polypeptide of the invention demonstrates cytosolic, antiarteriosclerotic, anticonvulsant, neurotrophic, neuroprotective, cerbroprotective, anti-HIV, anti-allergic, anti-inflammatory and thymolametic activities and may be useful for treating and diagnosing various disorders including those which are cell proliferative such as cancer and atherosclerosis, neurological including epilepsy, Huntington's disease and stroke, immune/inflammatory particularly AIDS and allergies and developmental such as hypothyroidism and Cushing's syndrome, as well as infections. The current sequence is that of the human REMAP protein of the invention.	The invention relates to a novel isolated polypeptide comprising a human receptor and membrane-associated protein (REMAP). The polypeptide of the invention demonstrates cytosolic, antiarteriosclerotic, anticonvulsant, neurotrophic, neuroprotective, cerbroprotective, anti-HIV, anti-allergic, anti-inflammatory and thymolametic activities and may be useful for treating and diagnosing various disorders including those which are cell proliferative such as cancer and atherosclerosis, neurological including epilepsy, Huntington's disease and stroke, immune/inflammatory particularly AIDS and allergies and developmental such as hypothyroidism and Cushing's syndrome, as well as infections. The current sequence is that of the human REMAP protein of the invention.	The invention relates to a novel isolated polypeptide comprising a human receptor and membrane-associated protein (REMAP). The polypeptide of the invention demonstrates cytosolic, antiarteriosclerotic, anticonvulsant, neurotrophic, neuroprotective, cerbroprotective, anti-HIV, anti-allergic, anti-inflammatory and thymolametic activities and may be useful for treating and diagnosing various disorders including those which are cell proliferative such as cancer and atherosclerosis, neurological including epilepsy, Huntington's disease and stroke, immune/inflammatory particularly AIDS and allergies and developmental such as hypothyroidism and Cushing's syndrome, as well as infections. The current sequence is that of the human REMAP protein of the invention.
XX	Sequence 172 AA;	Sequence 172 AA;	Sequence 172 AA;
XX	Query Match 100.0%; Score 106; DB 7; Length 172;	Query Match 100.0%; Score 106; DB 7; Length 172;	Query Match 100.0%; Score 106; DB 7; Length 172;
XX	Best Local Similarity 100.0%; Pred. No. 6.7e-08;	Best Local Similarity 100.0%; Pred. No. 6.7e-08;	Best Local Similarity 100.0%; Pred. No. 6.7e-08;
XX	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 106; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
|||||
DB 39 GFTNYTDFEDSPYFKENSA 57

RESULT 11
ADR65994
ID ADR65994 standard; protein; 214 AA.

XX AC ADR65994;

XX DT 02-DEC-2004 (first entry)

XX DE Human prostatic carcinoma derived protein SEQ ID 190 #1.

XX KW human; cytostatic; diagnosis; prostatic cancer;
XX KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.

XX PR 27-FEB-2003; 2003DE-01009985.

XX PR 14-MAY-2003; 2003DE-01022134.

XX PA (HINZ/) HINZMANN B.

XX PA (DAHL/) DAHL E.

XX PA (ROSE/) ROSENTHAL A.

XX PA (HERM/) HERMANN K.

XX PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
XX PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
XX PI Xinzhong L, Staub E;

XX DR WPI; 2004-653386/63.

XX PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
XX PT useful for diagnosis, treatment and in screening for specific binding
XX PT agents.

XX PS Claim 2; Page 585; 1607pp; German.

XX CC This invention describes novel cytostatic polynucleotide and polypeptide
XX CC sequences which can be used in a method for diagnosing prostatic cancer
XX CC or the risk of developing prostatic cancer. Diagnosis is based on
XX CC determining over transcription or over expression of the sequences in
XX CC prostatic tissue. Screening for inhibitors of the sequences or detection
XX CC substances involves a binding assay, any compounds that bind are
XX CC selected, optionally after deconvolution of mixtures. Detection of a
XX CC predetermined minimum level of the reporter indicates the presence of
XX CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
XX CC short-interfering RNA or ribozymes; an organic molecule of molecular
XX CC weight below 5000, preferably 300, that binds to the polypeptide; an
XX CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
XX CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
XX CC (monoclonal) antibody directed against Ab or any of the above derivatised
XX CC with a reporter group, cell toxin, immunostimulatory molecules and/or
XX CC radioisotope. The polynucleotides are identified in human prostatic
XX CC cancer by differential expression analysis, using DNA microarrays,
XX CC between normal and tumorous tissues, with (over)expression being detected
XX CC by quantitative PCR. Analysis of prostatic cancer samples showed that
XX CC CD24 was upregulated in many of them. Sections of tissue, isolated from
XX CC prostatic cancer patients, or subjects at risk, were incubated

CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65905-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
XX invention.

XX SQ Sequence 214 AA;

Query Match 100.0%; Score 106; DB 8; Length 214;

Best Local Similarity 100.0%; Pred. No. 8.5e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19

|||||

DB 124 GFTNYTDFEDSPYFKENSA 142

RESULT 12

ADR66892
ID ADR66892 standard; protein; 214 AA.

XX AC ADR66892;

XX DT 02-DEC-2004 (first entry)

XX DE Human prostatic carcinoma derived DNA SEQ ID 190 #4.

XX KW human; cytostatic; diagnosis; prostatic cancer;
XX KW differential expression analysis.

XX OS Homo sapiens.

XX PN WO2004076614-A2.

XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.

XX PR 27-FEB-2003; 2003DE-01009985.

XX PR 14-MAY-2003; 2003DE-01022134.

XX PA (HINZ/) HINZMANN B.

XX PA (DAHL/) DAHL E.

XX PA (ROSE/) ROSENTHAL A.

XX PA (HERM/) HERMANN K.

XX PA (PILA/) PILARSKY C.

XX PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
XX PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
XX PI Xinzhong L, Staub E;

XX DR WPI; 2004-653386/63.

XX PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
XX PT useful for diagnosis, treatment and in screening for specific binding
XX PT agents.

XX PS Claim 2; Page 1545; 1607pp; German.

XX CC This invention describes novel cytostatic polynucleotide and polypeptide
XX CC sequences which can be used in a method for diagnosing prostatic cancer
XX CC or the risk of developing prostatic cancer. Diagnosis is based on
XX CC determining over transcription or over expression of the sequences in
XX CC prostatic tissue. Screening for inhibitors of the sequences or detection
XX CC substances involves a binding assay, any compounds that bind are
XX CC selected, optionally after deconvolution of mixtures. Detection of a
XX CC predetermined minimum level of the reporter indicates the presence of
XX CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
XX CC short-interfering RNA or ribozymes; an organic molecule of molecular

weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, cancer by normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR5805-ADR6954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

CC Sequence 214 AA;

Query Match 100.0%; Score 106; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
Db 124 GFTNYTDFEDSPYFKENSA 142

RESULT 13

AAW75060
ID AAW75060 standard; protein; 233 AA.

XX AAW75060;

XX 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 4 clone HKCSR70.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; fetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Misc-difference 233

FT /label= unknown

XX WO9839446-A2.

XX 11-SEP-1998.

XX 06-MAR-1998; 98WO-US004482.

XX 07-MAR-1997; 97US-0038621P.

PR 07-MAR-1997; 97US-0040161P.

PR 07-MAR-1997; 97US-0040162P.

PR 07-MAR-1997; 97US-0040163P.

PR 07-MAR-1997; 97US-0040333P.

PR 07-MAR-1997; 97US-0040334P.

PR 07-MAR-1997; 97US-0040336P.

PR 11-APR-1997; 97US-0043311P.

PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-00433568P.
PR 11-APR-1997; 97US-00433569P.
PR 11-APR-1997; 97US-00433576P.
PR 11-APR-1997; 97US-00433578P.
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PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
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PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
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PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
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PR 22-AUG-1997; 97US-0056845P.
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PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.

Mon Feb 7 16:18:27 2005

PR 22-AUG-1997; 97US-0056632P.
 PR 22-AUG-1997; 97US-0056633P.
 PR 22-AUG-1997; 97US-0056637P.
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 PR 22-AUG-1997; 97US-0056910P.
 PR 22-AUG-1997; 97US-0056911P.
 PR 05-SEP-1997; 97US-0057650P.
 PR 05-SEP-1997; 97US-0057761P.
 PR 06-MAR-1998; 98WO-US004482.
 XX
 FA (RUBE/) RUBEN S M.
 FA (ROSE/) ROSEN C A.
 FA (FISC/) FISCHER C L.
 FA (SOPP/) SOPPET D R.
 FA (CART/) CARTER K C.
 FA (BEDN/) BEDNARIK D R.
 FA (ENDR/) ENDRESS G A.
 FA (YUGG/) YU G.
 FA (NIJJ/) NI J.
 FA (FENG/) FENG P.
 FA (YOUN/) YOUNG P E.
 FA (GREE/) GREENE J M.
 FA (FERR/) FERRIE A M.
 FA (DUAN/) DUAN R.
 FA (HUJJ/) HU J.
 FA (FLOR/) FLORENCE K A.
 FA (OLSE/) OLSEN H S.
 FA (EBNE/) EBNER R.
 FA (BREW/) BREWER L A.
 FA (SHIY/) SHI Y.
 XX
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
 PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Shi Y;
 XX
 DR WPI: 2003-466138/44.
 DR N-PSDB; ACD08028.
 XX
 PT Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
 PT or treating deficiencies or disorders of the immune system, autoimmune
 PT disorders, hyperproliferative disorders, and infectious diseases.
 XX
 PS Claim 11; Page 173; 243pp; English.
 XX
 CC The invention describes an isolated human secreted HODAZ50 polypeptide
 CC (I) comprising a sequence at least 95% identical to a sequence selected
 CC from polypeptide fragment of any one of the 123 polypeptide sequences

CC (PS) fully defined in the specification and having biological activity,
 CC polypeptide domain or epitope of PS, secreted form of PS, full-length
 CC protein of PS, or variant, allelic variant or species homologue of PS.
 CC (I) or a polynucleotide (II) encoding (I) is useful for preventing,
 CC treating, or ameliorating a medical condition in a mammalian subject. (I)
 CC or (II) is also useful for diagnosing a pathological condition or a
 CC susceptibility to a pathological condition in a subject. (I) is useful
 CC for identifying a binding partner which involves contacting the
 CC polypeptide with the binding partner and determining whether the binding
 CC partner affects the activity of the polypeptide. (I) or (II) is useful
 CC for diagnosing or treating deficiencies or disorders of the immune
 CC system, deficiencies or disorders of haematopoietic cells, to treat
 CC immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
 CC Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
 CC coagulation disorders, blood platelet disorders, autoimmune disorders
 CC (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
 CC dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
 CC graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms,
 CC located in the abdomen, bone, breast, digestive system, liver, pancreas,
 CC peritoneum, endocrine glands), infectious diseases (e.g., viral,
 CC bacterial, fungal or parasitic infection), central and peripheral nervous
 CC system diseases (e.g., spinal cord disorders, head trauma or stroke), to
 CC differentiate, proliferate and attract cells leading to the regeneration
 CC of tissues to repair, replace or protect tissue damaged by congenital
 CC defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
 CC osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
 CC is useful to modulate mammalian characteristics, to modulate mammalian
 CC metabolism affecting catabolism, anabolism, processing, utilisation, and
 CC storage of energy, to change a mammal's mental state or physical state,
 CC or as a food additive or preservative, such as to increase or decrease
 CC storage capabilities, fat content, lipid, protein, carbohydrate,
 CC vitamins, minerals, cofactors or other nutritional components. This is
 CC the amino acid sequence of a novel human secreted protein
 XX
 SQ Sequence 233 AA;
 Query Match 100.0%; Score 106; DB 6; Length 233;
 Best Local Similarity 100.0%; Pred. No. 9.3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTNYTDFEDSPYFKENSA 19
 DB 142 GFTNYTDFEDSPYFKENSA 160
 RESULT 15
 AAG62153
 ID AAG62153 standard; protein; 240 AA.
 XX
 AC AAG62153;
 XX
 DT 06-JUL-2001 (first entry)
 XX
 DE Human P503S inventive antigen SEQ ID NO: 352.
 XX
 KW Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.
 XX
 OS Homo sapiens.
 XX
 PN WO200125273-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US027465.
 XX
 PR 04-OCT-1999; 99US-0157459P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Xu J, Cheever MA, Reed SG;
 XX
 XX WPI: 2001-328324/34.

XX Polypeptide comprising part of the Wilms Tumor gene product sequence is
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1.
 XX

PS Disclosure; Page 223-224; 228pp; English.

XX
 CC The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WT1 and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WT1
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention
 XX

SQ Sequence 240 AA;

Query Match 100.0%; Score 106; DB 4; Length 240;
 Best Local Similarity 100.0%; Pred. No. 9.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 151 GFTNYTDFEDSPYKNSA 169

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 Job time : 100.508 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:50:20 ; Search time 24.1525 Seconds
(without alignments)
58.724 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169

Perfect score: 106

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgm2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgm2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgm2_6/ptodata/1/1aa/PTCUS_COMB.pep:*
- 6: /cgm2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	106	100.0	19	3	US-09-439-313-504
2	106	100.0	19	4	US-09-636-215-504
3	106	100.0	19	4	US-09-685-166A-504
4	106	100.0	19	4	US-09-679-426-504
5	106	100.0	19	4	US-09-759-143-504
6	106	100.0	19	4	US-09-651-236-504
7	106	100.0	233	4	US-09-148-545-137
8	106	100.0	241	3	US-08-808-148-1
9	106	100.0	241	3	US-09-020-956-114
10	106	100.0	241	3	US-09-030-607-114
11	106	100.0	241	3	US-09-439-313-114
12	106	100.0	241	3	US-09-352-616A-114
13	106	100.0	241	4	US-09-232-149A-114
14	106	100.0	241	4	US-09-159-812-114
15	106	100.0	241	4	US-09-636-215-114
16	106	100.0	241	4	US-09-685-166A-114
17	106	100.0	241	4	US-09-115-453-114
18	106	100.0	241	4	US-09-688-489-114
19	106	100.0	241	4	US-09-678-426-114
20	106	100.0	241	4	US-09-759-143-114
21	106	100.0	241	4	US-09-651-236-114
22	87	82.1	43	4	US-09-663-600A-129
23	87	82.1	43	4	US-09-663-600A-223
24	51	48.1	249	4	US-09-949-016-8334
25	49	46.2	252	3	US-08-705-771-17
26	49	46.2	252	4	US-09-417-540-17
27	45	42.5	223	4	US-09-270-767-61548

28	45	42.5	253	4	US-09-134-000C-6473	Sequence 6473, Ap
29	45	42.5	600	4	US-09-248-796A-23971	Sequence 23971, A
30	45	42.5	757	4	US-09-583-110-5096	Sequence 5096, Ap
31	45	42.5	778	4	US-09-107-433-5143	Sequence 5143, Ap
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33	43	40.6	94	4	US-09-513-999C-4913	Sequence 4913, Ap
34	43	40.6	225	4	US-09-513-999C-4168	Sequence 4168, Ap
35	43	40.6	202	4	US-09-949-016-8347	Sequence 8347, Ap
36	43	40.6	260	4	US-09-949-016-7296	Sequence 7296, Ap
37	43	40.6	267	4	US-09-949-016-9088	Sequence 9088, Ap
38	43	40.6	270	4	US-09-949-016-9117	Sequence 9117, Ap
39	43	40.6	275	4	US-09-949-016-8346	Sequence 8346, Ap
40	43	40.6	366	4	US-09-543-681A-7506	Sequence 7506, Ap
41	43	40.6	809	1	US-07-789-915A-4	Sequence 4, Appli
42	43	40.6	809	1	US-08-005-002C-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1

US-09-439-313-504

; Sequence 504, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqui

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fangter, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439.313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 504

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-439-313-504

Query Match 100.0%; Score 106; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19

DB 1 GFTNYTDFEDSPYFKENSA 19

RESULT 2

US-09-636-215-504

; Sequence 504, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

```

; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 19
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-636-215-504

Query Match      100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19

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; Sequence 504, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-685-166A-504

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Query Match      100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 4
US-09-679-426-504
; Sequence 504, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-679-426-504

Query Match      100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 5
US-09-759-143-504
; Sequence 504, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick

```

APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 504
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-759-143-504

Query Match 100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
|||||
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 6
US-09-651-236-504
Sequence 504, Application US/09651236
Patent No. 6818751
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 504
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-651-236-504

Query Match 100.0%; Score 106; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 7
US-09-148-545-137
Sequence 137, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
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; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
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; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

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Query Match 100.0%; Score 106; DB 4; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GFTNYTDFEDSPYFKENSA 19
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Db 142 GFTNYTDFEDSPYFKENSA 160
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RESULT 8
US-08-808-148-1
; Sequence 1, Application US/08808148
; Patent No. 6020478
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer

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APPLICANT: Goli, Surya
 APPLICANT: Zhang, Hong wolfe
 TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-SEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/808,148
 FILING DATE: Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0218 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PROSNOT26
 CLONE: 2187263

US-08-808-148-1

Query Match 100.0%; Score 106; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 151 GFTNYTDFEDSPYFKENSA 169

RESULT 9

US-09-020-956-114
 Sequence 114, Application US/09020956
 Patent No. 6261562
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 178
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/020,956
 FILING DATE: 09-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 114:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-020-956-114

Query Match 100.0%; Score 106; DB 3; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
 Db 151 GFTNYTDFEDSPYFKENSA 169

RESULT 10

US-09-030-607-114
 Sequence 114, Application US/09030607
 Patent No. 6262245
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangchun
 APPLICANT: Dillon, Davin C.
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 NUMBER OF SEQUENCES: 224
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/030,607
 FILING DATE: 25-FEB-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.427C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 114:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-09-030-607-114

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Query Match      100.0%; Score 106; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYFKENSA 19
Db      151 GFTNYTDFEDSPYFKENSA 169

RESULT 11
US-09-439-313-114
; Sequence 114, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-439-313-114

Query Match      100.0%; Score 106; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYFKENSA 19
Db      151 GFTNYTDFEDSPYFKENSA 169

RESULT 12
US-09-352-616A-114
; Sequence 114, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-352-616A-114

Query Match      100.0%; Score 106; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GFTNYTDFEDSPYFKENSA 19
Db      151 GFTNYTDFEDSPYFKENSA 169

RESULT 13
US-09-232-149A-114
; Sequence 114, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-232-149A-114

Query Match      100.0%; Score 106; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYFKENSA 19
Db      151 GFTNYTDFEDSPYFKENSA 169

RESULT 14
US-09-159-812-114
; Sequence 114, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-159-812-114

Query Match      100.0%; Score 106; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYFKENSA 19
Db      151 GFTNYTDFEDSPYFKENSA 169

RESULT 15
US-09-636-215-114
; Sequence 114, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

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; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-114

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Query Match      100.0%; Score 106; DB 4; Length 241;
Best Local Similarity 100.0%; Pred.No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GFTNYTDFEDSPYFKNSA 19
    |||||
Db 151 GFTNYTDFEDSPYFKNSA 169

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Search completed: February 5, 2005, 20:07:13
Job time : 25.1525 secs

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Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 2
US-09-780-669-504
; Sequence 504, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-780-669-504

Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 3
US-09-822-827-504
; Sequence 504, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-822-827-504

Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 4
US-09-895-793-504
; Sequence 504, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-895-793-504

Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 5
US-09-995-814-504
; Sequence 504, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 2
US-09-780-669-504
; Sequence 504, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-780-669-504

Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 3
US-09-822-827-504
; Sequence 504, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-822-827-504

Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 4
US-09-895-793-504
; Sequence 504, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-780-669-504

Query Match 100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
| | | | | | | | | | | | | | | | | | | | |
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 5
US-09-995-814-504
; Sequence 504, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

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; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-895-814-504

Query Match      100.0%; Score 106; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKNSA 19
Db      1 GFTNYTDFEDSPYFKNSA 19

RESULT 6
US-10-012-896-504
; Sequence 504, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
```

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; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-012-896-504

Query Match      100.0%; Score 106; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKNSA 19
Db      1 GFTNYTDFEDSPYFKNSA 19

RESULT 7
US-10-010-940-504
; Sequence 504, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-010-940-504

Query Match      100.0%; Score 106; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKNSA 19
Db      1 GFTNYTDFEDSPYFKNSA 19

RESULT 8
US-10-144-678A-504
; Sequence 504, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
```

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; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144.678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-144-678A-504

Query Match 100.0%; Score 106; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19
Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 9
US-10-294-025-504
; Sequence 504, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294.025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-294-025-504

Query Match 100.0%; Score 106; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENSA 19

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Db 1 GFTNYTDFEDSPYFKENSA 19

RESULT 10
US-09-981-876-137
; Sequence 137, Application US/09981876
; Patent No. US20020184689A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,598
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,632

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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
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; PRIOR APPLICATION NUMBER: 60/056,631
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; PRIOR FILING DATE: 1997-08-22

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; PRIOR APPLICATION NUMBER: 60/056,908
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

Query Match 100.0%; Score 106; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
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Db 142 GFTNYTDFEDSPYFKENSA 160

RESULT 11
US-09-148-545-137
; Sequence 137, Application US/09148545

Publication No. US20030027132A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 137
LENGTH: 233

Query Match 100.0%; Score 106; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 142 GFTNYTDFEDSPYFKENSA 160
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RESULT 12

US-10-264-237-1489
Sequence 1489, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1489
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-237-1489

Query Match 100.0%; Score 106; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 150 GFTNYTDFEDSPYFKENSA 168
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RESULT 13

US-09-759-143-114
Sequence 114, Application US/09759143
Patent No. US2002022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 114
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapien
US-09-759-143-114

Query Match 100.0%; Score 106; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFKENSA 19
Db 151 GFTNYTDFEDSPYFKENSA 169
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RESULT 14

US-09-780-669-114
Sequence 114, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.

```

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Sreiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-114

Query Match      100.0%; Score 106; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKENSA 19
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Db      151 GFTNYTDFEDSPYFKENSA 169

Search completed: February 5, 2005, 20:11:30
Job time : 71.1695 secs

; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-606-114

Query Match      100.0%; Score 106; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GFTNYTDFEDSPYFKENSA 19
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Db      151 GFTNYTDFEDSPYFKENSA 169

Search completed: February 5, 2005, 20:11:30
Job time : 71.1695 secs

; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Sreiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
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US-09-780-669-114

Query Match      100.0%; Score 106; DB 9; Length 241;
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Db      151 GFTNYTDFEDSPYFKENSA 169

RESULT 15
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; Sequence 114. Application US/09030606
; Patent No. US20020081580A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,606
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.428C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:49:45 ; Search time 18.678 Seconds
(without alignments)
97.876 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169

Perfect score: 106
Sequence: 1 GFTNYTDFSDSPYFKENSA 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	51	48.1	244	1 I39368	T-cell acute lymph
3	49	46.2	253	2 A59264	tetraspan TSPAN-3
4	46.5	43.9	644	2 E88487	protein Cl3B9.4 [i
5	46	43.4	379	1 RGKLA	GTP-binding regula
6	45	42.5	308	2 AE2960	hypothetical prote
7	45	42.5	319	2 A98323	ABC transporter, p
8	45	42.5	322	2 AB2078	iron(III) dicitrat
9	45	42.5	401	2 H97714	apartate transami
10	45	42.5	431	2 T38260	hypothetical prote
11	45	42.5	648	2 B84139	ABC transporter (p
12	45	42.5	757	2 D95103	x-pro dipeptidyl-p
13	45	42.5	795	2 B97971	x-pro dipeptidyl-p
14	45	42.5	1403	2 I40325	dermonecrotic loxi
15	44.5	42.0	459	2 AD1787	lysine decarboxyla
16	44	41.5	203	2 D84221	hypothetical prote
17	44	41.5	384	2 T44652	UNP-N-acetylglucos
18	44	41.5	1069	2 C85349	Ca2+-transporting
19	44	41.5	1093	2 T08551	Ca2+-transporting
20	43.5	41.0	1941	2 T23979	hypothetical prote
21	43.5	41.0	1943	2 T23986	hypothetical prote
22	43	40.6	98	2 S26932	Ig heavy chain V r
23	43	40.6	238	1 I38016	melanoma-associate
24	43	40.6	245	2 A59258	tetraspan TSPAN-6
25	43	40.6	552	2 T37424	hypothetical prote
26	43	40.6	684	2 T37944	hypothetical prote
27	43	40.6	729	2 F83725	hypothetical prote
28	43	40.6	773	2 A71079	probable transcrip
29	43	40.6	773	2 D75031	hydrogenase expres

30	43	40.6	809	2 S67665	ubiquitin-specific
31	43	40.6	1162	2 T21557	hypothetical prote
32	43	40.6	1599	2 S22737	glucosyltransferas
33	43	40.6	4351	2 T00252	MEGF1 protein - ra
34	42	39.6	59	2 C64024	hypothetical prote
35	42	39.6	243	2 AE1709	FMN-containing NAD
36	42	39.6	245	2 A59260	tetraspan TSPAN-6
37	42	39.6	247	2 T50286	hypothetical prote
38	42	39.6	370	2 F86338	protein F2D10.2 [i
39	42	39.6	402	2 A86194	hypothetical prote
40	42	39.6	458	2 T47389	hypothetical prote
41	42	39.6	567	2 JC4714	alpha-glucosidase
42	42	39.6	644	2 T08340	probable arsenical
43	42	39.6	735	2 AC0858	conserved hypothet
44	41.5	39.2	353	2 AD1384	aldose 1-epimerase
45	41.5	39.2	827	2 S59121	SOX6 protein - mou

ALIGNMENTS

RESULT 1

A59262

Tetraspan TSPAN-1 - human

C:Species: Homo sapiens (man)

C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C/Accession: A59262

R:Todd, S.C.; Doctor, V.S.; Levy, S.

Biochim. Biophys. Acta 1399, 101-104, 1998

A>Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.

A/Reference number: A59258; MUID:98390278; PMID:9714763

A/Accession: A59262

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-241 <TOD>

A/Cross-references: UNIPROT:O60635; GB:AF054838; NID:g2997740; PIDN:AAC69714.1; PID:g299

C/Genetics:

A/Gene: TSPAN-1

C/Superfamily: CD9 antigen

Query Match 100.0%; Score 106; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. NO. 4.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTNYTDFSDSPYFKENSA 19

Db 151 GFTNYTDFSDSPYFKENSA 169

RESULT 2

I39368

T-cell acute lymphoblastic leukemia associated antigen 1 - human

N/Alternate names: cell surface glycoprotein (clone A15); TALLA-1

C:Species: Homo sapiens (man)

C>Date: 23-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 22-Jun-1999

C/Accession: I39368; I54784

R:Emi, N.; Kikaoxi, K.; Seto, M.; Ueda, R.; Saito, H.; Takahashi, T.

Immunogenetics 37, 193-198, 1993

A>Title: Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfa

A/Reference number: I39368; MUID:93131291; PMID:8420826

A/Accession: I39368

A/Molecule type: mRNA

A/Residues: 1-244 <RES>

A/Cross-references: GB:D10653; NID:g285900; PIDN:BAA01501.1; PID:g285901

A/Experimental source: immature T cell line HPB-ALL

R:Takagi, S.; Fujikawa, K.; Imai, T.; Fukuhara, N.; Fukudome, K.; Minegishi, M.; Tsuchiy

Int. J. Cancer 61, 706-715, 1995

A>Title: Identification of a highly specific surface marker of T-cell acute lymphoblasti

A/Reference number: I54784; MUID:95286314; PMID:7768645

A/Accession: I54784

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-244 <RE2>

Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A.Reference number: A75000; MUID:99069613; PMID:9851916
A.Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.elegans/
A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 282, 2012-2018, 1998
A.Accession: E8467
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-544 <STO>
A.Cross-references: UNIPROT:Q09460; GB:chr_III; PIN:AAA62517.1; PID:9687811; GSPDB:GN0000000000; C:Genetics;

A:Accession
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <NR>
A:Cross-references: UNIPROT:Q8UNT4; GB:AE008689; PID:AAI44099.1; PID:gl7741667; GSPDB:CN
A:Experimental source: strain C58 (Dupont)
C:Genetics
C:Gene: malF
A:Map position: linear chromosome
C:Superfamily: inner membrane protein ugpA

```
Query Match      42.5%; Score 45; DB 2; Length 308;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENS 18
    |||||
Db 71 GFENYTMFDDPIFWETT 88

RESULT 7
A98323
ABC transporter, permease protein, malFg family [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A98323
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A98323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <KUR>
A:Cross-references: UNIPROT:Q8UAT4; GB:AE007870; PIDN:AAK90107.1; PID:gl5160096; GSPDB:G
C:Genetics:
A:Gene: AGR_L_3068
A:Map position: linear chromosome
C:Superfamily: inner membrane protein ugpA

Query Match      42.5%; Score 45; DB 2; Length 319;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKENS 18
    |||||
Db 82 GFENYTMFDDPIFWETT 99

RESULT 8
AB2078
iron(III) dicitrate-binding protein of ABC transporter alr2176 [imported] - Nostoc sp.
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AB2078
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 203-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-322 <KUR>
A:Cross-references: UNIPROT:Q8YV05; GB:BA000019; PIDN:BAB73875.1; PID:gl7131267; GSPDB:G
C:Genetics:
A:Experimental source: strain PCC 7120
A:Gene: alr2176
C:Superfamily: ferrichrome-iron transport protein fecB

Query Match      42.5%; Score 45; DB 2; Length 322;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 FTNYTDFEDSPYFKEN 17
    :|||
Db 150 YPNYTMVLVDQAFKEN 165

RESULT 9
H97714
aspartate transaminase (EC 2.6.1.1) - Rickettsia conorii (strain Malish 7)
```

```
C:Species: Rickettsia conorii
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: H97714
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: H97714
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <KUR>
A:Cross-references: UNIPROT:Q92JE7; GB:AE006914; PIDN:AAI02658.1; PID:gl5619162; GSPDB:G
C:Genetics:
A:Gene: aatA
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match      42.5%; Score 45; DB 2; Length 401;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFTNYTDFEDSPYFKES 16
    |||||
Db 60 GFTKYTNVEGMPLLKQ 75

RESULT 10
T38260
hypothetical protein SPAC23C4.05c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38260
R:Harris, D.; Squares, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: 221782
A:Accession: T38260
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-431 <HAR>
A:Cross-references: UNIPROT:O94559; EMBL:299753; PIDN:CAB16876.1; GSPDB:GN00066; SPDB:SP
A:Experimental source: strain 972h-; cosmid C23C4
C:Genetics:
A:Gene: SPDB:SPAC23C4.05c
A:Map position: 1
A:Introns: 23/1

Query Match      42.5%; Score 45; DB 2; Length 431;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 TNVTDFEDSPYFKES 16
    |||||
Db 231 TNITDSQPAPYKKE 244

RESULT 11
B84139
ABC transporter (permease) BH3914 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B84139
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, N.; Masui, R.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B84139
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-648 <STO>
A:Cross-references: UNIPROT:Q9K618; GB:AP001520; GB:BA000004; NID:gl0176401; PIDN:BA0076
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3914
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```
Query Match      42.5%; Score 45; DB 2; Length 648;
Best Local Similarity 72.7%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 TDFSDSPYFKE 16
      |||:|||||
Db      332 TDMEDAAAYFKE 342
      |||:|||||

RESULT 12
D95103
X-pro dipeptidyl-peptidase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: D95103
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidorn, J.D.; Umayam, L.A.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95103
A:Status: preliminary
A:Superfamily: Lactococcus X-Pro dipeptidyl-peptidase
A:Molecule type: DNA
A:Residues: 1-757 <KUR>
A:Cross-references: UNIPROT:Q97RC9; GB:AE005672; PIDN:AAK75021.1; PID:gl14972369; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0894
C:Superfamily: Lactococcus X-Pro dipeptidyl-peptidase

Query Match      42.5%; Score 45; DB 2; Length 757;
Best Local Similarity 44.4%; Pred. No. 53;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYFKENS 18
      |||:|||||
Db      90 GFSYLVDFEDSDVFRKET 107
      |||:|||||

RESULT 13
B97971
X-pro dipeptidyl-peptidase (EC 3.4.14.11) [imported] - Streptococcus pneumoniae (strain B97971)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: B97971
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Hee, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21423245; PMID:11544234
A:Accession: B97971
A:Status: preliminary
A:Superfamily: Lactococcus X-Pro dipeptidyl-peptidase
A:Molecule type: DNA
A:Residues: 1-795 <KUR>
A:Cross-references: UNIPROT:Q8DQ87; GB:AE007317; PIDN:AAK99598.1; PID:gl15458392; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: pepXP
C:Superfamily: Lactococcus X-Pro dipeptidyl-peptidase
C:Keywords: dipeptidylpeptide hydrolase

Query Match      42.5%; Score 45; DB 2; Length 795;
Best Local Similarity 44.4%; Pred. No. 56;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYFKENS 18
      |||:|||||
Db      128 GFSYLVDFEDSDVFRKET 145
      |||:|||||
```

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RESULT 14
I40325
dermonecrotic toxin - Bordetella pertussis
C:Species: Bordetella pertussis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C/Accession: I40325
R:Walker, K.E.; Weiss, A.A.
Infect. Immun. 62, 3817-3828, 1994
A:Title: Characterization of the Dermonecrotic Toxin in the Genus Bordetella.
A:Reference number: I40325; MUID:94341887; PMID:8063398
A:Accession: I40325
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1451 <RES>
A:Cross-references: UNIPROT:Q45336; EMBL:U10527; NID:gs523316; PIDN:AAA20995.1; PID:gs5233
C:Genetics:
A:Gene: dnt

Query Match      42.5%; Score 45; DB 2; Length 1451;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 GFTNYTDFEDSPYF 14
      |||:|||||
Db      427 GFISPTDFRSDAF 440
      |||:|||||

RESULT 15
ADI1787
lysine decarboxylase homolog lin2842 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 28-Jul-2003
C/Accession: ADI1787
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species.
A:Reference number: ABI077; MUID:21537279; PMID:11679669
A:Accession: ADI1787
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC98068.1; PID:gl16415377; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2842
C:Superfamily: lysine decarboxylase

Query Match      42.0%; Score 44.5; DB 2; Length 459;
Best Local Similarity 52.6%; Pred. No. 36;
Matches 10; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY      1 GFTNY---TDFEDSPYFKE 16
      |||:|||||
Db      316 GYTGVELQTFESSYFPE 334
      |||:|||||

Search completed: February 5, 2005, 20:05:44
Job time : 20.678 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:36:20 ; Search time 90.1695 Seconds
(without alignments)
107.902 Million cell updates/sec

Title: US-09-780-669-114_COPY_151_169

Perfect score: 106

Sequence: 1 GFTNYTDFSDSPYFKNSA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	241	1	TSN1 HUMAN
2	62	58.5	241	2	O6AYR9 rattus norv
3	60	56.6	240	2	O99J59 mus musculus
4	56	52.8	248	2	O810P9 mus musculus
5	52	49.1	96	2	Q7VAG9 Qvags prochloroco
6	51	48.1	52	2	Q7Z215 homo sapien
7	51	48.1	52	2	Q7YQH1 Q7yqh1 pan troglod
8	51	48.1	52	2	Q7YQH2 Q7yqh2 pan troglod
9	51	48.1	240	2	O6GPI1 Q6gpi1 xenopus lae
10	51	48.1	244	1	T4S2_PANTR
11	51	48.1	244	1	T4S2_PONPY
12	51	48.1	244	2	Q7Z326
13	51	48.1	249	1	T4S2 HUMAN
14	50	47.2	433	2	O89XR2 Q89xr2 bradyrhizob
15	50	47.2	434	2	O6N118 rhodopsendo
16	50	47.2	728	2	Q9UWN8 sulfolobus
17	49	46.2	157	2	Q8R0G6 Q8r0g6 mus musculus
18	49	46.2	235	2	Q7RD42 Q7rd42 plasmodium
19	49	46.2	240	2	Q6P420 xenopus lae
20	49	46.2	244	2	Q6PDN6 Q6pdn6 mus musculus
21	49	46.2	244	2	O6DDV1 Q6ddv1 xenopus lae
22	49	46.2	245	2	Q8BPV2 Q8bpv2 mus musculus
23	49	46.2	249	1	T4S2_MOUSE
24	49	46.2	253	1	T4S8 HUMAN
25	49	46.2	253	1	T4S8_MOUSE
26	49	46.2	253	2	Q66H06 Q66h06 rattus norv
27	49	46.2	254	2	O8ILA9 Q8ila9 plasmodium
28	49	46.2	424	2	Q89GR4 Q89gr4 bradyrhizob
29	48.5	45.8	234	2	Q7T2B8 Q7t2b8 brachydanio
30	48	45.3	157	2	Q9GMU7 Q9gm7 macaca fasc
31	48	45.3	506	2	Q8S2J1 Q8s2j1 oryza sativ

32 48 45.3 790 2 Q6FR86 Q6fr86 candida gla
33 47 44.3 186 2 Q8R8J0 Q8r8j0 thermocaneer
34 47 44.3 194 2 Q67QV1 Q67qv1 symbiobacte
35 47 44.3 328 2 Q976G5 Q976g5 sulfolobus
36 47 44.3 340 2 Q95XK8 Q95xk8 caenothabdi
37 46.5 43.9 495 2 Q8PSR6 Q8psr6 xanthomonas
38 46 43.4 109 2 Q9L7X0 Q9l7x0 clostridium
39 46 43.4 258 2 Q94F78 Q94f78 zea mays (m
40 46 43.4 271 2 Q89PB4 Q89pe4 bradyrhizob
41 46 43.4 299 2 Q88TV7 Q88tv7 lactobacill
42 46 43.4 323 2 Q7Q3Z8 Q7q3z8 anopholes g
43 46 43.4 379 1 GBAS_XENLA P24799 xenopus lae
44 46 43.4 384 2 Q7MZG8 Q7mzg8 photorhabdu
45 46 43.4 412 2 Q8XJJ0 Q8xjj0 clostridium

ALIGNMENTS

RESULT 1
TSN1 HUMAN
ID TSN1 HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Tetraspanin 1 (Tspan-1) (Tetraspanin NET-1) (Tetraspanin TM4-C).
GN Name="TSPAN1";
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TM4SF family.";
RL Biochim. Biophys. Acta 1399:101-104(1998).
[2]
RP SEQUENCE FROM N.A.
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database.";
[3]
RP Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspanins.";
[4]
RP Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
TC TISSUE=Colon;
RX MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Goughman J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RA	Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E.,
RA	Jones S.J., Marra M.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RC	Director MGC Project;
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC078938; AAT78938.1; -
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	InterPro; IPR002229; RhesusRHD.
DR	InterPro; IPR008952; Tetraspanin.
DR	InterPro; IPR000301; Transmem.4.
DR	PFam; PF00335; Tetraspanin; 1.
DR	PRINTS; PR00342; RHESUSRHD.
DR	PRINTS; PR00259; TMFOUR.
DR	PROSITE; PS00421; TM4.1; 1.
SQ	SEQUENCE 241 AA; 26453 MW; 9118E865464D1A70 CRC64;
Query Match 58.5%; Score 62; DB 2; Length 241;	
Best Local Similarity 64.7%; Pred. No. 0.15;	
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps	
Qy	1 GFTNYTDRDPSYFKEN 17
Db	151 GFNYTDFNSSRFVKEN 167
RESULT 3	
Q99J59	PRELIMINARY; PRT; 240 AA.
ID	Q99J59
AC	Q99J59;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	RIKEN cDNA 9030418M05 [Mus musculus adult male colon cDNA, RIKEN full-
DE	length enriched library, clone:9030418M05 product:similar to tetraspan
DE	TSpan-1]
DE	TSpan-1]
GN	Name=9030418M05Rik;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NMRI; TISSUE=Mammary tumor;
RC	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RC	STrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marinus K., Farmer A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA	Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Richards S., Rhee K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC003448; AA003448.1; -;
DR EMBL; AK078869; BAC37431.1; -;
DR MGI; MGI:1914055; 9030418M05Rik.

DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem.4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00342; RHESUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TW4.1; 1.
SQ SEQUENCE 240 AA; 26356 MW; AD4C448A32BC2999 CRC64;

Query Match 56.6%; Score 60; DB 2; Length 240;
Best Local Similarity 64.7%; Pred. No. 0.32;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GFTVNTDFEDSPYFKEN 17
||| ||||| : |||
Db 151 GFNNYTFNARSFVKEN 167

RESULT 4
Q810P9 PRELIMINARY; PRT; 248 AA.
AC Q810P9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049650; AA049650.1; -;
GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem.4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
KW Hypothetical protein.
SQ SEQUENCE 248 AA; 27877 MW; F89C7B36382E2C5B CRC64;

Query Match 52.8%; Score 56; DB 2; Length 248;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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aps 0;
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Db          5 GVQNTNWTSTSPYFLEH 21

RESULT 8
Q7YQH2
ID Q7YQH2 PRELIMINARY; PRT; 52 AA.
AC Q7YQH2
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transmembrane 4 superfamily member 2 (Fragment).
GN Name=TW4SP2;
OS Pan troglodytes troglodytes.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=37011;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees.";
RL Mol. Biol. Evol. 20:1281-1289(2003).
DR EMBL; AB102484; BAC80953.1; -
DR EMBL; AB102485; BAC80954.1; -
DR EMBL; AB102486; BAC80955.1; -
DR EMBL; AB102487; BAC80956.1; -
DR EMBL; AB102488; BAC80957.1; -
DR EMBL; AB102489; BAC80958.1; -
DR EMBL; AB102490; BAC80959.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR003031; Transmem.4.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5774 MW; 420AB346A5074DC8 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 52;
Best Local Similarity 52.9%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFLEN 17
| | | | | | | | | |
Db 5 GVQNTNWTSTSPYFLEH 21

RESULT 9
Q6GP11
ID Q6GP11 PRELIMINARY; PRT; 240 AA.
AC Q6GP11
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC80751 protein.
GN Name=MGC80751;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubinger R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Splice;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Splice;
RA Klein S., Gerhard D.S.;
RL EMBL; BC073338; AAH73338.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR003031; Transmem.4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
SQ SEQUENCE 240 AA; 26875 MW; 96475F0A8F920998 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 240;
Best Local Similarity 42.1%; Pred. No. 8.4;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GFTNYTDFEDSPYFLEN 19
| | | | | | | | | |
Db 146 GRKNTDWEETDWTNNKS 164

RESULT 10
T4S2_PANTR
ID T4S2_PANTR STANDARD; PRT; 244 AA.
AC Q7YQL0;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane 4 superfamily member 2.
GN Name=TW4SP2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees.";
RL Mol. Biol. Evol. 20:1281-1289(2003).
CC -!- FUNCTION: May be involved in cell proliferation and cell motility.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILILAR LOCATION: Belongs to the tetraspanin (TW4SF) family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements/

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OCOS Homo sapiens (Human).
OCOC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OCOC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OCOC

RP SEQUENCE FROM N.A.
RC STRAIN=USD110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohata M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USD110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005935; BAC45510.1; -.
DR HSSP; P13254; 1GCO.
DR GO; GO:0016829; F-lyase activity; IEA.
DR GO; GO:0016765; F:transferase activity, transferring alkyl or. . .; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000277; Cys Met Meta PP.
DR InterPro; IPR006235; OAH_OAS_sulphy.
DR Pfam; PF01053; Cys Met Meta PP; 1.
DR TIGRFAMs; TIGR01326; OAH_OAS_sulphy; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 433 AA; 46823 MW; 5A4110C4615F70B5 CRC64;

Query Match 47.2%; Score 50; DB 2; Length 433;
Best Local Similarity 61.5%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FTNYTDFEDSPYF 14
Db : ||| | ||| :
313 WVNVTGFPDSPY 325

RESULT 15
Q6N118
ID Q6N118 PRELIMINARY; PRT; 434 AA.
AC Q6N118;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Homocysteine synthase (EC 2.5.1.49).
GN Names:metY; OrderedLocusNames:RPA4591;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572607; CAE30031.1; -.
DR GO; GO:0003951; P:O-acetylhomoserine aminocarboxypropyltransf. . .; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000277; Cys Met Meta PP.
DR InterPro; IPR006235; OAH_OAS_sulphy.
DR Pfam; PF01053; Cys Met Meta PP; 1.
DR TIGRFAMs; TIGR01326; OAH_OAS_sulphy; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 434 AA; 46947 MW; B7846EA96BA911FC CRC64;

Query Match 47.2%; Score 50; DB 2; Length 434;
Best Local Similarity 61.5%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FTNYTDFEDSPYF 14
Db : ||| | ||| :
313 WVNVTGFPDSPY 325

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:34:18 ; Search time 104.746 Seconds
(without alignments)
73.847 Million cell updates/sec

Title: US-09-780-669-114_COPY_165_184
Perfect score: 116
Sequence: 1 KENSAFPFCCNDNVNTAN 20

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*1: Geneseqp1980s:*2: Geneseqp1990s:*3: Geneseqp2000s:*4: Geneseqp2001s:*5: Geneseqp2002s:*6: Geneseqp2003as:*7: Geneseqp2003bs:*8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	20	4	AAM01158 Human pro
2	116	100.0	20	4	AAU69803 Human pro
3	116	100.0	20	4	AAG99043 Human pro
4	116	100.0	20	4	ABU71694 Prostate
5	116	100.0	20	5	ABR5263 Epitope m
6	116	100.0	20	6	ABR54375 Prostate
7	116	100.0	20	7	ADB13955 Human pro
8	116	100.0	20	7	ADG26371 Human pro
9	116	100.0	172	7	ADD69590 Human REM
10	116	100.0	174	8	ADP81123 Protein o
11	116	100.0	214	8	ADR65994 Human pro
12	116	100.0	214	8	ADR66892 Human pro
13	116	100.0	233	6	AAW75060 Human sec
14	116	100.0	233	6	ABO01936 Novel hum
15	116	100.0	240	4	AAAG62153 Human pol
16	116	100.0	240	5	ABR89113 Human pol
17	116	100.0	241	2	AAW63386 Prostate
18	116	100.0	241	2	AAW59954 Amino aci
19	116	100.0	241	2	AAW71870 Amino aci
20	116	100.0	241	2	AAW58380 Human sec
21	116	100.0	241	3	AAW82003 Human imm
22	116	100.0	241	3	ABG94412 Human pro
23	116	100.0	241	4	AAM01118 Human pro
24	116	100.0	241	4	AAU69764 Human pro
25	116	100.0	241	4	AAB74801 Prostate

26	116	100.0	241	4	AAG999003 Human pro
27	116	100.0	241	4	ABU71654 Prostate
28	116	100.0	241	4	AAB90679 Human AR4
29	116	100.0	241	4	AAU04962 Human pro
30	116	100.0	241	5	ABG96434 Human ova
31	116	100.0	241	5	ABG95223 Human NI-
32	116	100.0	241	5	ABG76666 Prostate
33	116	100.0	241	6	ABR54335 Prostate
34	116	100.0	241	7	ADB75601 Prostate
35	116	100.0	241	7	ADB13564 Human pro
36	116	100.0	241	7	ADG25980 Human pro
37	116	100.0	241	7	ADN33286 Cancer/An
38	116	100.0	258	5	ABG96433 Human ova
39	116	100.0	258	7	ADB75599 Prostate
40	116	100.0	273	2	AAW61618 Clone HPW
41	116	100.0	273	7	ABW01500 Human rec
42	50	43.1	241	5	ABR09512 Human TSP
43	50	43.1	241	8	ADO10063 Novel hum
44	50	43.1	301	7	ADG44848 S. solfat
45	50	43.1	301	7	ADG42862 S. solfat

ALIGNMENTS

RESULT 1
AAM01158
ID AAM01158 standard; peptide; 20 AA.

AC AAM01158;

XX 04-OCT-2001 (first entry)

XX Human prostate-specific peptide used in epitope mapping studies #15.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis.

XX Homo sapiens.

XX WO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001WO-US001574.

XX 14-JAN-2000; 2000US-00483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
XX Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
XX Wang A, Meagher MJ;
XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
XX vaccines.

XX Claim 2; Page 399; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX prepared using (I) or (II) are used to treat cancer in a patient. (I) and
XX the antibodies are also used in the detection of cancer in a patient. The
XX cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX and (II) can be used in vaccines. The antibodies or (I) can be used for
XX monitoring the progression of cancer in a patient. (I) and (II) can also
XX be used to improve diagnostic and therapeutic methods for prostate
XX cancer. They can indicate the level of metastasis as well as the prostate

CC prostate cancer therapy associated peptide. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX ABU71694 standard; peptide; 20 AA.

AC ABU71694;

XX 10-JUN-2003 (first entry)

XX Prostate cancer therapy associated peptide #16.

XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA.

XX Homo sapiens.

XX US2002192763-A1.

XX 19-DEC-2002.

XX 29-JUN-2001; 2001US-00895793.

XX 04-OCT-1999; 99US-0157455P.

XX 04-OCT-2000; 2000US-00679272.

XX 28-MAR-2001; 2001US-00822827.

XX (XUJJ/) XU J.

XX (DILL/) DILLON D C.

XX (MITC/) MITCHAM J L.

XX (HARL/) HARLOCKER S L.

XX (JIAN/) JIANG Y.

XX (KALO/) KALOS M D.

XX (FANG/) FANGER G R.

XX (RETT/) RETTER M W.

XX (STOL/) STOLK J A.

XX (DAYC/) DAY C H.

XX (VEDV/) VEDVICK T S.

XX (CART/) CARTER D.

XX (LISX/) LI S X.

XX (WANG/) WANG A.

XX (SKEI/) SKEIKY Y A W.

XX (HEPL/) HEPLER W T.

XX (HEND/) HENDERSON R A.

XX (HURA/) HURAL J.

XX (MCNE/) MCNEILL P D.

XX (HOUG/) HOUGHTON R L.

XX (DBAS/) Y DE BASSOLS C V.

XX (FOYT/) FOY T M.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;

XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.

XX Example 18; SEQ ID NO 505; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 35 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This is the amino acid sequence of a

SQ Sequence 20 AA;

Query Match 100.0%; Score 116; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAFPFPCCNDNVNTAN 20

Db 1 KENSAFPFPCCNDNVNTAN 20

RESULT 5

ABB95263

ID ABB95263 standard; peptide; 20 AA.

XX AC ABB95263;

XX DT 19-JUL-2002 (first entry)

XX DE Epitope mapping study peptide SEQ ID NO 505.

XX KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
 KW gene therapy.

XX OS Unidentified.

XX PN US2002022248-A1.

XX PD 21-FEB-2002.

XX PF 12-JAN-2001; 2001US-00759143.

XX 25-FEB-1997; 97US-00806099.

XX 01-AUG-1997; 97US-00904804.

XX 10-FEB-1998; 98US-00020956.

XX 25-FEB-1998; 98US-00030807.

XX 14-JUL-1998; 98US-00115453.

XX 23-SEP-1998; 98US-00159812.

XX 15-JAN-1999; 99US-00232149.

XX 09-APR-1999; 99US-0028946.

XX 13-JUL-1999; 99US-00352616.

XX 12-NOV-1999; 99US-00439313.

XX 18-NOV-1999; 99US-00443686.

XX 14-JAN-2000; 2000US-00483672.

XX 27-MAR-2000; 2000US-00536857.

XX 09-MAY-2000; 2000US-00568100.

XX 12-MAY-2000; 2000US-00570737.

XX 13-JUN-2000; 2000US-00593793.

XX 27-JUN-2000; 2000US-00605783.

XX 10-AUG-2000; 2000US-00636215.

XX 29-AUG-2000; 2000US-00651236.

XX 06-SEP-2000; 2000US-00657279.

XX 02-OCT-2000; 2000US-00679426.

XX 10-OCT-2000; 2000US-00685166.

XX (XUJJ/) XU J.

XX (DILL/) DILLON D C.

XX (MITC/) MITCHAM J L.

XX (HARL/) HARLOCKER S L.

XX (JIAN/) JIANG Y.

XX (KALO/) KALOS M D.

XX (FANG/) FANGER G R.

XX (RETT/) RETTER M W.

XX (STOL/) STOLK J A.

XX (DAYC/) DAY C H.

XX (VEDV/) VEDVICK T S.

XX (CART/) CARTER D.

XX (LISX/) LI S X.

PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 505; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a
CC peptide described in the invention
XX
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 116; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-10; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KENSARPPFCNDNVNTAN 20
Db 1 KENSARPPFCNDNVNTAN 20
RESULT 6
ABR54375
ID ABR54375 standard; protein; 20 AA.
AC ABR54375;
XX
XX 28-AUG-2003 (first entry)
XX
XX Prostate tumour specific related peptide for epitope mapping SEQ ID 505.
XX
XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer.
XX
XX Homo sapiens.
OS
XX WO200289747-A2.
XX
XX 14-NOV-2002.
XX
XX 09-MAY-2002; 2002WO-US014753.
XX
XX 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX

PS Example 18; Page 466; 69lpp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 116; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-10; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KENSARPPFCNDNVNTAN 20
Db 1 KENSARPPFCNDNVNTAN 20
RESULT 7
ABR13955
ID ABR13955 standard; peptide; 20 AA.
XX
XX ABR13955;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human prostate protein P503S epitope mapping peptide #2102.
XX
XX Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
KW cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell; epitope.
XX
XX Homo sapiens.
OS
XX US2003185830-A1.
XX
XX 02-OCT-2003.
XX
XX 12-NOV-2002; 2002US-00294025.
XX
XX 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX

Db 1 KENSAPFPCCNDNVNTAN 20
|||||

RESULT 9
ID ADD69590 standard; protein; 172 AA.

AC ADD69590;

XX 15-JAN-2004 (first entry)

DE Human REMAP protein - SEQ ID 19.

XX human; receptor and membrane-associated protein; REMAP; cytostatic;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; antiallergic; antiinflammatory;
KW thymimetic; cell proliferative; cancer; atherosclerosis; neurological;
KW epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS;
KW allergy; developmental; hypothyroidism; Cushing's syndrome; infection.

OS Homo sapiens.

XX WO2003048305-A2.

PN 12-JUN-2003.

XX 13-NOV-2002; 2002WO-US036759.

XX 13-NOV-2001; 2001US-0333097P.

XX 15-NOV-2001; 2001US-0335274P.

XX 14-DEC-2001; 2001US-0340542P.

XX 18-DEC-2001; 2001US-0342166P.

XX 11-JAN-2002; 2002US-0347580P.

XX 14-JAN-2002; 2002US-0348687P.

XX (INCY-) INCYTE GENOMICS INC.

PI Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y,
PI Chawla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM;
PI Thangavelu K, Lee S, Emmerling BM, Kable AE, Khare R, Baughn MR;
PI Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ;
PI Lee EA, Swarnakar A, Kallick DA, Griffin JA, Elliott VS, Gorvad AE;
PI Hatalla AA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U;
PI Burrill JD, Blake JJ, Ho A, Zheng W, Gao J;

XX WPI; 2003-513744/48.

DR N-PSDB; ADD69637.

XX New human receptors and membrane-associated proteins (REMAP), useful for
PT diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
PT infections.

PS Claim 1; SEQ ID NO 19; 298pp; English.

XX The invention relates to a novel isolated polypeptide comprising a human
CC receptor and membrane-associated protein (REMAP). The polypeptide of the
CC invention demonstrates cytostatic, antiarteriosclerotic, anticonvulsant,
CC nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,
CC antiinflammatory and thymimetic activities and may be useful for
CC treating and diagnosing various disorders including those which are cell
CC proliferative such as cancer and atherosclerosis, neurological including
CC epilepsy, Huntington's disease and stroke, immune/inflammatory
CC particularly AIDS and allergies and developmental such as hypothyroidism
CC and Cushing's syndrome, as well as infections. The current sequence is
CC that of the human REMAP protein of the invention.

XX Sequence 172 AA;

Query Match 100.0%; Score 116; DB 7; Length 172;
Best Local Similarity 100.0%; Fred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ov 1 KENSAPFPCCNDNVNTAN 20
|||||
Db 96 KENSAPFPCCNDNVNTAN 115

RESULT 10

ID ADP81123 standard; protein; 174 AA.

XX ADP81123;

XX 09-SEP-2004 (first entry)

XX Protein of human ovarian specific gene, SEQ ID No 157.

XX normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
KW metastatic; cancer; vaccine; cytostatic; human.

XX Homo sapiens.

XX WO2004053079-A2.

XX 24-JUN-2004.

XX 08-DEC-2003; 2003WO-US038855.

XX 06-DEC-2002; 2002US-0431301P.

XX 06-DEC-2002; 2002US-0431321P.

PR 30-JUN-2003; 2003US-0484584P.

XX 07-NOV-2003; 2003US-0518607P.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Turner LR, Sun Y, Liu S, Chen H;

XX WPI; 2004-468850/44.

XX N-PSDB; ADP80988.

XX Claim 12; SEQ ID NO 157; 754pp; English.

XX The invention relates to novel isolated nucleic acid molecules and
CC polypeptides present in normal and neoplastic ovarian cells. These
CC comprise a nucleic acid sequence encoding any of the 167 amino acid
CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
CC specification (SEQ. ID NOS: ADP81095 to ADP81261) and comprises any of
CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
CC in the specification (SEQ. ID NOS: ADP80967 to ADP81094). The invention
CC further comprises: a method for determining the presence of an ovarian
CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
CC nucleic acid molecule; a host cell comprising the vector; a method for
CC producing a polypeptide encoded by the above nucleic acid molecule; a
CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
CC or its fragment that specifically binds to the above polypeptide; a
CC method for determining the presence of an ovarian specific protein in a
CC sample; a method for diagnosing or monitoring the presence and metastases
CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
CC presence of cancer in a patient; the kit comprising a means for
CC determining the presence of the above nucleic acid molecule or
CC polypeptide; a method of treating a patient with ovarian cancer; and a
CC vaccine comprising the above polypeptide or nucleic acid encoding the
CC polypeptide. The isolated nucleic acid molecules and polypeptides have
CC cytostatic activity. The isolated polypeptides may be used to create a
CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
CC for diagnosing or monitoring the presence and metastases of ovarian
CC cancer and treating ovarian cancer. This sequence represents the protein
CC of an ovarian specific gene of the invention.

XX Sequence 174 AA;

Query Match 100.0%; Score 116; DB 8; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNSAFPPPCNDNVNTNAN 20
| | | | | | | | | | | | | | | | | | | | | |
DB 53 KNSAFPPPCNDNVNTNAN 72

RESULT 11
ADR65994
ID ADR65994 standard; protein; 214 AA.
XX
AC ADR65994;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived protein SEQ ID 190 #1.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX
OS Homo sapiens.
XX
FN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pillarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhang L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
agents.
XX
PS Claim 2; Page 585; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated

CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.

SQ Sequence 214 AA;
Query Match 100.0%; Score 116; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNSAFPPPCNDNVNTNAN 20
| | | | | | | | | | | | | | | | | | | | | |
DB 138 KNSAFPPPCNDNVNTNAN 157

RESULT 12
ADR66892
ID ADR66892 standard; protein; 214 AA.
XX
AC ADR66892;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 190 #4.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis.
XX
OS Homo sapiens.
XX
FN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pillarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhang L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
agents.
XX
PS Claim 2; Page 1545; 1607pp; German.
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular

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us-09-780-669-114_copy_165_184.rag

CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies:
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR5805-ADR6954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 116; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSARPPFCNDNVNTAN 20
Db 138 KENSARPPFCNDNVNTAN 157
|||||

RESULT 13
AAW75060
ID AAW75060 standard; protein; 233 AA.

XX AAW75060;

XX 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 4 clone HKCSR70.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; fetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Misc-difference 233
FT /label= unknown

XX WO9839446-A2.

XX 11-SEP-1998.

XX 06-MAR-1998; 98WO-US004482.

XX 07-MAR-1997; 97US-0038621P.

PR 07-MAR-1997; 97US-0040161P.

PR 07-MAR-1997; 97US-0040162P.

PR 07-MAR-1997; 97US-0040163P.

PR 07-MAR-1997; 97US-0040333P.

PR 07-MAR-1997; 97US-0040334P.

PR 07-MAR-1997; 97US-0040336P.

PR 11-APR-1997; 97US-0040626P.

PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
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PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
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PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 22-AUG-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
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PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.

PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JW;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX WPI; 1998-609887/51.
DR N-PSDB; AAV34157.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 1; Page 281-282; 447pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34145) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 70 novel
CC genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC acid sequences AAW75057-W75179) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 70 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 233 AA;

Query Match 100.0%; Score 116; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
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Db 156 KENSAPPPFCNDNVNTAN 175

RESULT 14
ABO01936
ID ABO01936 standard; protein; 233 AA.
XX
XX ABO01936;
AC
XX
XX 12-AUG-2003 (first entry)
DT
XX
XX Novel human secreted protein #4.
XX
XX Human; immunoglobulin G; IgG; fragment of crystallisation; Fc;
KW immune system disorder; haematopoietic cell disorder;
KW immunologic deficiency disorder; ataxia telangiectasia; HIV infection;
KW Wiskott-Aldrich disorder; thrombocytopenia; haemoglobinuria;
KW blood coagulation disorder; blood platelet disorder; autoimmune disorder;
KW Addison's disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
KW glomerulonephritis; Grave's disease; allergic reaction;
KW graft-versus-host disease; hyperproliferative disorder; neoplasm;
KW infectious disease; nervous system disease; spinal cord disorder;

KW head trauma; stroke; tissue regeneration; congenital defect; trauma;
KW wound; burn; incision; ulcer; age disease; osteoporosis;
KW periodontal disease; liver failure; catabolism; anabolism; metabolism;
KW food additive; preservative; secreted protein.
XX
XX Homo sapiens.
XX
XX US2003027132-A1.
XX
XX 06-FEB-2003.
XX
XX 04-SEP-1998; 98US-00148545.
XX
XX 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 07-MAR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
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PR 11-APR-1997; 97US-0043569P.
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PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
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PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.

22-AUG-1997; 97US-0056632P.
 22-AUG-1997; 97US-0056636P.
 22-AUG-1997; 97US-0056637P.
 22-AUG-1997; 97US-0056662P.
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 22-AUG-1997; 97US-0056862P.
 22-AUG-1997; 97US-0056864P.
 22-AUG-1997; 97US-0056872P.
 22-AUG-1997; 97US-0056874P.
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 22-AUG-1997; 97US-0056876P.
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 22-AUG-1997; 97US-0056909P.
 22-AUG-1997; 97US-0056910P.
 22-AUG-1997; 97US-0056911P.
 05-SEP-1997; 97US-0057650P.
 05-SEP-1997; 97US-0057761P.
 06-MAR-1998; 98WO-US004482.
 (RUBE/) RUBEN S M.
 (ROSE/) ROSEN C A.
 (RISC/) FISCHER C L.
 (SOPP/) SOPPET D R.
 (CART/) CARTER K C.
 (BEDN/) BEDNARIK D R.
 (ENDR/) ENDRESS G A.
 (YUGG/) YU G.
 (NIJJ/) NI J.
 (FENG/) FENG P.
 (YOUN/) YOUNG P E.
 (GREE/) GREENE J M.
 (FERR/) FERRIE A M.
 (DUAN/) DUAN R.
 (HUJJ/) HU J.
 (FLOR/) FLORENCE K A.
 (OLSE/) OLSEN H S.
 (EBNE/) EBNER R.
 (BREW/) BREWER L A.
 (SHIY/) SHI Y.
 Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
 Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA,
 Shi Y;
 WPI: 2003-466138/44.
 N-PSDB; ACD08028.
 Novel isolated human secreted HODAZ50 polypeptide useful for diagnosing
 or treating deficiencies or disorders of the immune system, autoimmune
 disorders, hyperproliferative disorders, and infectious diseases.
 Claim 11; Page 173; 243pp; English.
 The invention describes an isolated human secreted HODAZ50 polypeptide
 (I) comprising a sequence at least 95% identical to a sequence selected
 from polypeptide fragment of any one of the 123 polypeptide sequences

CC (PS) fully defined in the specification and having biological activity,
 CC polypeptide domain or epitope of PS, secreted form of PS, full-length
 CC protein of PS, or variant, allelic variant or species homologue of PS.
 CC (I) or a polynucleotide (II) encoding (I) is useful for preventing,
 CC treating, or ameliorating a medical condition in a mammalian subject. (I)
 CC or (II) is also useful for diagnosing a pathological condition or a
 CC susceptibility to a pathological condition in a subject. (I) is useful
 CC for identifying a binding partner which involves contacting the
 CC polypeptide with the binding partner and determining whether the binding
 CC partner affects the activity of the polypeptide. (I) or (II) is useful
 CC for diagnosing or treating deficiencies or disorders of the immune
 CC system, deficiencies or disorders of haematopoietic cells, to treat
 CC immunologic deficiency disorders, ataxia telangiectasia, HIV infection,
 CC Wiskott-Aldrich disorders, thrombocytopenia or haemoglobinuria, blood
 CC coagulation disorders, blood platelet disorders, autoimmune disorders
 CC (e.g., Addison's disease, haemolytic anaemia, rheumatoid arthritis,
 CC dermatitis, glomerulonephritis, Grave's disease), allergic reactions,
 CC graft-versus-host disease, hyperproliferative disorders (e.g., neoplasms,
 CC located in the abdomen, bone, breast, digestive system, liver, pancreas,
 CC peritoneum, endocrine glands), infectious diseases (e.g., viral,
 CC bacterial, fungal or parasitic infection), central and peripheral nervous
 CC system diseases (e.g., spinal cord disorders, head trauma or stroke), to
 CC differentiate, proliferate and attract cells leading to the regeneration
 CC of tissues to repair, replace or protect tissue damaged by congenital
 CC defects, trauma (wounds, burns, incisions, or ulcers) age disease (e.g.,
 CC osteoporosis, periodontal disease, liver failure) or surgery. (I) or (IV)
 CC is useful to modulate mammalian characteristics, to modulate mammalian
 CC metabolism affecting catabolism, anabolism, processing, utilisation, and
 CC storage of energy, to change a mammal's mental state or physical state,
 CC or as a food additive or preservative, such as to increase or decrease
 CC storage capabilities, fat content, lipid, protein, carbohydrate,
 CC vitamins, minerals, cofactors or other nutritional components. This is
 CC the amino acid sequence of a novel human secreted protein
 XX Sequence 233 AA;
 SQ

Query Match 100.0%; Score 116; DB 6; Length 233;
 Best Local Similarity 100.0%; Pred. No. 4.8e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KENSAPPPPCNDNVNTNTAN 20
 DB 156 KENSAPPPPCNDNVNTNTAN 175
 RESULT 15
 AAG62153
 ID AAG62153 standard; protein; 240 AA.
 XX
 AC AAG62153;
 XX
 DT 06-JUL-2001 (first entry)
 XX
 DE Human P5038 inventive antigen SEQ ID NO: 352.
 XX
 KW Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
 XX chromosome 11p13; zinc finger transcription factor.
 OS Homo sapiens.
 XX
 PN WO200125273-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US027465.
 XX
 PR 04-OCT-1999; 99US-0157459P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAW, Xu J, Cheever MA, Reed SG;
 XX WPI: 2001-328324/34.
 DR

XX Polypeptide comprising part of the Wilms Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WT1.
XX
PS Disclosure; Page 223-224; 228pp; English.
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WT1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WT1
CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukaemia. The present sequence is
CC a polypeptide described in the exemplification of the invention
XX
SQ Sequence 240 AA;
Query Match 100.0%; Score 116; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KENSAPPPCCNDNVNTAN 20
| | | | | | | | | | | | | | | | | | | | | |
Db 165 KENSAPPPCCNDNVNTAN 184
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Job time : 104.746 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 20:00:18 ; Search time 74.9153 Seconds
(without alignments)
86.952 Million cell updates/sec

Title: US-09-780-669-114_COPY_165_184

Perfect score: 116

Sequence: 1 KENSAFFPFCNDNVNTAN 20

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	100.0	20	9	US-09-759-143-505
2	116	100.0	20	9	US-09-780-669-505
3	116	100.0	20	9	US-09-822-827-505
4	116	100.0	20	9	US-09-895-793-505
5	116	100.0	20	9	US-09-895-814-505
6	116	100.0	20	13	US-10-012-896-505
7	116	100.0	20	14	US-10-010-940-505
8	116	100.0	20	14	US-10-144-678A-505
9	116	100.0	20	14	US-10-294-025-505
10	116	100.0	233	9	US-09-981-876-137
11	116	100.0	233	10	US-09-148-545-137
12	116	100.0	241	15	US-10-264-237-1489
13	116	100.0	241	9	US-09-759-143-114

14	116	100.0	241	9	US-09-780-669-114
15	116	100.0	241	9	US-09-030-606-114
16	116	100.0	241	9	US-09-822-827-114
17	116	100.0	241	9	US-09-115-453-114
18	116	100.0	241	9	US-09-232-880-114
19	116	100.0	241	9	US-09-908-193-44
20	116	100.0	241	9	US-09-895-793-114
21	116	100.0	241	9	US-09-895-814-114
22	116	100.0	241	13	US-10-012-896-114
23	116	100.0	241	14	US-10-097-340-326
24	116	100.0	241	14	US-10-010-940-114
25	116	100.0	241	14	US-10-205-823-425
26	116	100.0	241	14	US-10-144-678A-114
27	116	100.0	241	14	US-10-294-025-114
28	116	100.0	241	15	US-10-295-027-604
29	116	100.0	241	15	US-10-037-417-77
30	116	100.0	241	15	US-10-037-417-78
31	116	100.0	241	16	US-10-888-838-114
32	116	100.0	258	14	US-10-097-340-324
33	116	100.0	258	14	US-10-205-823-423
34	116	100.0	273	14	US-10-156-136-20
35	50	43.1	92	16	US-10-437-963-189981
36	50	43.1	240	9	US-09-908-193-43
37	50	43.1	240	10	US-09-823-187-74
38	50	43.1	240	15	US-10-037-417-76
39	50	43.1	241	15	US-10-037-417-22
40	50	43.1	301	15	US-10-299-867-21
41	50	43.1	544	16	US-10-450-156-1
42	48	41.4	49	9	US-09-864-761-39257
43	47	40.5	165	15	US-10-424-599-249829
44	46.5	40.1	74	14	US-10-316-253-58
45	46.5	40.1	1887	10	US-09-853-180-3

ALIGNMENTS

RESULT 1

US-09-759-143-505
; Sequence 505, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Steiky, Yasir A.W.
; APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759.143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 505
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-759-143-505

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Query Match      100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KENSAPPFCCNDNVNTAN 20
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RESULT 2
US-09-780-669-505
; Sequence 505, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-780-669-505

Query Match      100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KENSAPPFCCNDNVNTAN 20
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RESULT 3
US-09-822-827-505
; Sequence 505, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-822-827-505

Query Match      100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPFCCNDNVNTAN 20
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Db 1 KENSAPPFCCNDNVNTAN 20
   |||||

RESULT 4
US-09-895-793-505
; Sequence 505, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895.793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-895-793-505

Query Match      100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPFCCNDNVNTAN 20
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Db 1 KENSAPPFCCNDNVNTAN 20
   |||||

RESULT 5
US-09-895-814-505
; Sequence 505, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
```

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-895-814-505

Query Match 100.0%; Score 116; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
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Db 1 KENSAPPPFCNDNVNTAN 20

RESULT 6
US-10-012-896-505
; Sequence 505, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro

; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-012-896-505

Query Match 100.0%; Score 116; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
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Db 1 KENSAPPPFCNDNVNTAN 20

RESULT 7
US-10-010-940-505
; Sequence 505, Application US/10010940
; Publication No. US20030089062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-010-940-505

Query Match 100.0%; Score 116; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
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Db 1 KENSAPPPFCNDNVNTAN 20

RESULT 8
US-10-144-678A-505
; Sequence 505, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.

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; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-144-678A-505

Query Match 100.0%; Score 116; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAFPFFCCNDNVNTAN 20
Db 1 KENSAFPFFCCNDNVNTAN 20

RESULT 9
US-10-294-025-505
; Sequence 505, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 20
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-294-025-505

Query Match 100.0%; Score 116; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAFPFFCCNDNVNTAN 20
Db 1 KENSAFPFFCCNDNVNTAN 20

RESULT 10
US-09-981-876-137
; Sequence 137, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT FILING DATE: 2001-10-19
; CURRENT APPLICATION NUMBER: US/09/981,876
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
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; PRIOR APPLICATION NUMBER: 60/038,621
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/043,314
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; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
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; PRIOR APPLICATION NUMBER: 60/043,671
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/056,631
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 05-Sep-1997
; PRIOR APPLICATION NUMBER: 60/047,599
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; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

Query Match 100.0%; Score 116; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KENSAPPPFCNDNVNTAN 20
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Db 156 KENSAPPPFCNDNVNTAN 175

RESULT 11
US-09-148-545-137
; Sequence 137, Application US/09148545

Mon Feb 7 16:18:31 2005

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; Publication No.: US20030027132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/043,576
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; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
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; EARLIER APPLICATION NUMBER: 60/056,664
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; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233
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Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      156 KENSAPPPFCNDNVNTAN 175
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RESULT 12
US-10-264-237-1489
; Sequence 1489, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P413P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
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; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1489
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-1489
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Best Local Similarity 100.0%; Pred. No. 1.6e-09;
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Db      164 KENSAPPPFCNDNVNTAN 183
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RESULT 13
US-09-759-143-114
; Sequence 114, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-114
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Query Match          100.0%; Score 116; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      165 KENSAPPPFCNDNVNTAN 184
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RESULT 14
US-09-780-669-114
; Sequence 114, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
```

APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 114
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapien
US-09-780-669-114

Query Match 100.0%; Score 116; DB 9; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAFPFFCCNDNVNTAN 20
Db 165 KENSAFPFFCCNDNVNTAN 184

Search completed: February 5, 2005, 20:11:31
Job time : 75.9153 secs

LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-606-114

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-09-030-606-114
Sequence 114. Application US/09030606
Patent No. US20020081580A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030.606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:

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3	51	44.0	860	1	VCLEJ4	env polyprotein pr
4	50	43.1	301	2	S75391	probable methionyl
5	50	43.1	566	2	S19307	carboxylesterase (
6	48	41.4	1293	2	S42402	xeroderma pigmento
7	46	39.7	194	2	F64598	modulator of drug
8	46	39.7	633	2	T04179	hypothetical prote
9	46	39.7	859	1	VCLJ22	env polyprotein pr
10	46	39.7	859	1	VCLJ21	env polyprotein pr
11	46	39.7	859	1	VCLJE1	env polyprotein pr
12	46	39.7	859	1	VCLJE2	env polyprotein pr
13	46	39.7	859	1	VCLJE3	env polyprotein pr
14	46	39.7	859	1	VCLJEV	env polyprotein pr
15	46	39.7	859	1	VCLJEW	env polyprotein pr
16	45	38.8	128	2	T15101	env polyprotein pr
17	45	38.8	145	2	T49328	hypothetical prote
18	45	38.8	196	2	T09968	hypothetical prote
19	45	38.8	460	2	C27311	cyclin-dependent k
20	45	38.8	463	2	T09968	NADH2 dehydrogenas
21	44.5	38.4	218	2	A11744	B. subtilis Yund p
22	44.5	38.4	363	2	F69325	hypothetical prote
23	44	37.9	279	2	B71415	first mannosyl tra
24	44	37.9	298	2	E85166	probable phosphoch
25	44	37.9	996	2	S70646	probable phosphoch
26	43	37.1	68	2	AB0417	transcription fact
27	43	37.1	194	2	A71915	conserved hypothet
28	43	37.1	241	2	S42436	hypothetical prote
29	43	37.1	304	2	S12975	proteasome endopep
30	43	37.1	304	2	S12975	coatprotein - pot


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RESULT 7
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modulator of drug activity - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: F64598
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, G.G.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 368, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64598
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-194 <TM>
A:Cross-references: UNIPROT:O25347; GB:AE000577; GB:AE000511; NID:g2313747; PIDN:AA0769
C:Superfamily: NAD(P)H dehydrogenase (quinone) 2

Query Match          39.7%; Score 46; DB 2; Length 194;
Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 SAPPFPCNDNVN 17
Db 161 SALPTFCNDVVKN 174

RESULT 8
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hypothetical protein F7L13.20 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04179
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15184
A:Accession: T04179
A:Molecule type: DNA
A:Residues: 1-633 <BEV>
A:Cross-references: UNIPROT:Q9S2X8; EMBL:AL049524
A:Experimental source: cultivar Columbia; BAC clone F7L13
C:Genetics:
A:Map position: 4
A:Introns: 224/3; 295/1; 394/2; 550/2
A>Note: F7L13.20

Query Match          39.7%; Score 46; DB 2; Length 633;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KENSAPFPFCNDN 14
Db 376 KQNNKSPPICSDN 389

RESULT 9
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env polyprotein precursor - equine infectious anemia virus (strain CL22)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp45; coat protein gp90
C:Species: equine infectious anemia virus
A>Note: host Equus caballus (domestic horse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: C41991
R:Perry, S.T.; Flaherty, M.T.; Kelley, M.J.; Clabough, D.L.; Tronick, S.R.; Coggins, L.;
J. Virol. 66, 4085-4097, 1992
A>Title: The surface envelope protein gene region of equine infectious anemia virus is r
A:Reference number: A41991; MUID:92292230; PMID:1318398
A:Accession: C41991

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A:Molecule type: DNA
A:Residues: 1-859 <PER>
A:Cross-references: UNIPROT:P32541; GB:MB7581; NID:g290627; PIDN:AAA43005.1; PID:g290630
C:Genetics:
A:Gene: env
C:Superfamily: equine infectious anemia virus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-859/Product: env polyprotein #status predicted <ENV>
F:23-444/Product: coat protein gp90 #status predicted <GPP>
F:445-859/Product: coat protein gp45 #status predicted <GGP>
F:446-472/Region: hydrophobic
F:615-636/Domain: transmembrane #status predicted <TMN>
F:40,112,141,148,186,214,233,244,340,368,399,406,411,483,490,550,557/Binding site: carbo
Query Match          39.7%; Score 46; DB 1; Length 859;
Best Local Similarity 38.9%; Pred. No. 48;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KENSAPFPFCNDNVN 18
Db 28 EENTMFQPCYNDSKNS 45

RESULT 10
VCLJE1
env polyprotein precursor (clone P3.2-1) - equine infectious anemia virus
N:Contains: coat protein gp45; coat protein gp90
C:Species: equine infectious anemia virus
A>Note: host Equus caballus (domestic horse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A34027
R:Payne, S.L.; Fang, F.D.; Liu, C.P.; Dhruva, B.R.; Rambo, P.; Issel, C.J.; Montelaro,
Virology 161, 321-331, 1987
A>Title: Antigenic variation and lentivirus persistence: variations in envelope gene seq
A:Reference number: A34027; MUID:88072070; PMID:2825406
A:Accession: A34027
A:Molecule type: genomic RNA
A:Residues: 1-859 <PAY>
A:Cross-references: UNIPROT:P22427; GB:M18385; NID:g323830; PIDN:AAA66407.1; PID:g323831
C:Genetics:
A:Gene: env
C:Superfamily: equine infectious anemia virus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-444/Product: coat protein gp90 #status predicted <CPI>
F:775-93/Domain: transmembrane #status predicted <TM1>
F:445-859/Product: coat protein gp45 #status predicted <CP2>
F:446-462/Domain: transmembrane #status predicted <TM2>
F:614-636/Domain: transmembrane #status predicted <TM3>
F:787-807/Domain: transmembrane #status predicted <TM4>
F:816-835/Domain: transmembrane #status predicted <TM5>
F:40,112,141,148,186,214,233,244,340,368,399,406,411,422,483,490,550,557,752/Binding sit
Query Match          39.7%; Score 46; DB 1; Length 859;
Best Local Similarity 38.9%; Pred. No. 48;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KENSAPFPFCNDNVN 18
Db 28 EENTMFQPCYNDSKNS 45

RESULT 11
VCLJE2
env polyprotein precursor (clone P3.2-2) - equine infectious anemia virus
N:Contains: coat protein gp45; coat protein gp90
C:Species: equine infectious anemia virus
A>Note: host Equus caballus (domestic horse)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: B34027
R:Payne, S.L.; Fang, F.D.; Liu, C.P.; Dhruva, B.R.; Rambo, P.; Issel, C.J.; Montelaro,
Virology 161, 321-331, 1987

```

C/Species: equine infectious anemia virus

Query Match 39.7%; Score 46; DB 1; Length 859;
Best Local Similarity 38.9%; Pred. No. 48;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Search completed: February 5, 2005, 20:05:45
Job time : 20.661 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2005, 19:36:20 ; Search time 94.9153 Seconds
(without alignments)
107.902 Million cell updates/sec

Title: US-09-780-669-114_COPY_165_184

Perfect score: 116

Sequence: 1 KENSAFPFPCCNDNVTNAN 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	241	1	TSN1_HUMAN
2	65	56.0	241	2	Q6AYR9
3	53	45.7	282	2	Q86FC1
4	51	44.0	91	2	Q6J758
5	51	44.0	91	2	Q6J763
6	51	44.0	91	2	Q6J766
7	51	44.0	91	2	Q6J767
8	51	44.0	91	2	Q6J768
9	51	44.0	91	2	Q6J769
10	51	44.0	108	1	RODL_NEUCR
11	51	44.0	860	1	ENV_EFV5
12	51	44.0	863	2	Q6AXF9
13	51	44.0	923	2	Q91X64
14	50	43.1	91	2	Q6J765
15	50	43.1	240	2	Q9J759
16	50	43.1	301	1	AMPM_SULSO
17	50	43.1	489	2	Q651F0
18	50	43.1	565	2	Q97582
19	50	43.1	566	1	EST1_PIG
20	49.5	42.7	850	2	Q70014
21	49	42.2	91	1	NLT1_PRUDU
22	48	41.4	810	2	Q6NBT3
23	48	41.4	888	2	Q6LST1
24	48	41.4	1293	1	XPC_DROME
25	48	41.4	1293	2	Q9U321
26	48	41.4	1293	2	Q9V7A8
27	48	41.4	1294	2	Q8MLA2
28	48	41.4	1623	2	Q7PDV5
29	47	40.5	297	2	Q6QW8
30	47	40.5	375	2	Q6EH13
31	46	39.7	66	2	Q66747

32	46	39.7	74	2	Q85499
33	46	39.7	90	2	Q8H2B2
34	46	39.7	91	1	NLT1_PRUAR
35	46	39.7	91	1	NLT1_PRUPE
36	46	39.7	91	2	Q9LED1
37	46	39.7	117	1	NLT1_PRUDU
38	46	39.7	123	2	Q6Z9S7
39	46	39.7	194	2	O25347
40	46	39.7	234	2	P88309
41	46	39.7	234	2	P88310
42	46	39.7	234	2	P88311
43	46	39.7	234	2	P88316
44	46	39.7	248	2	P88312
45	46	39.7	248	2	P88313

ALIGNMENTS

RESULT 1
TSN1_HUMAN
ID TSN1_HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tetraspanin 1 (Tspan-1) (Tetraspanin NET-1) (Tetraspanin TW4-C).
GN Name=TSpan1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TW4SF family.";
RL Biochim. Biophys. Acta 1399:101-104(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database.";
RN [3]
RP SEQUENCE FROM N.A.
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspans.";
RN [4]
RP SEQUENCE FROM N.A.
RA TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC -----
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 CC EMBL; AF054838; AAC69714.1; -
 CC EMBL; AF065388; AAC17119.1; -
 CC EMBL; AF133425; AAF08364.1; -
 CC EMBL; BC007290; AAH07290.1; -
 CC EMBL; BC013404; AAH13404.1; -
 CC PIR; A59262; A59262.
 CC H-InvDB; HIX0000543; -
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC InterPro; IPR008952; Tetraspanin.
 CC InterPro; IPR000301; Transmem_4.
 CC Pfam; PF00335; Tetraspanin; 1.
 CC PRINTS; PR00259; TMFOUR.
 CC PROSITE; PS00421; TM4.1; FALSE_NEG.
 KW Glycoprotein; Transmembrane.
 FT DOMAIN 1 11
 FT TRANSMEM 12 32 Cytoplasmic (Potential).
 FT DOMAIN 33 52 Potential.
 FT TRANSMEM 33 52 Extracellular (Potential).
 FT TRANSMEM 53 73 Potential.
 FT DOMAIN 74 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 109 Potential.
 FT DOMAIN 110 211 Extracellular (Potential).
 FT TRANSMEM 212 232 Potential.
 FT DOMAIN 233 241 Cytoplasmic (Potential).
 FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 189 189 K -> E (in Ref.1).
 SQ SEQUENCE 241 AA; 26301 MW; AF938AD7147CB884 CRC64;

Query Match 100.0%; Score 116; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 3.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KENSAPPPCCNDNVNTAN 20
 |||||
 DB 165 KENSAPPPCCNDNVNTAN 184
 |||||

RESULT 2
 Q6AYR9 PRELIMINARY; PRT; 241 AA.
 AC Q6AYR9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Tetraspanin 1.
 GN Name=MGC93753;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC078938; AAH78938.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR002229; RhesusRHD.
 DR InterPro; IPR008952; Tetraspanin.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Tetraspanin; 1.
 DR PRINTS; PR00342; RhesusRHD.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4.1; 1.
 SQ SEQUENCE 241 AA; 26453 MW; 9118E865464D1A70 CRC64;

Query Match 56.0%; Score 65; DB 2; Length 241;
 Best Local Similarity 71.4%; Pred. No. 0.043;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KENSAPPPCCNDN 14
 |||||
 DB 165 KENKVFPPPCANN 178
 |||||

RESULT 3
 Q86FC1 PRELIMINARY; PRT; 282 AA.
 AC Q86FC1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Clone ZD391 mRNA sequence.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
 RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
 RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
 RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
 RA Xue C.L., Feng Z., Chen Z., Han Z.G.;
 RT "Evolutionary and biomedical implications of a Schistosoma japonicum
 RT complementary DNA resource";
 RL Nat. Genet. 35:139-147 (2003).
 DR EMBL; AY222942; AAP05954.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Tetraspanin; 1.
 SQ SEQUENCE 282 AA; 31153 MW; 6CB2B4D2ED2B37C4 CRC64;

Query Match 45.7%; Score 53; DB 2; Length 282;
 Best Local Similarity 66.7%; Pred. No. 3.9;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 NSAPPPCCNDN 14
 |||||

DB 198 NSKYPFCCKFN 209

RESULT 4

Q6J758 PRELIMINARY; PRT; 91 AA.

AC Q6J758;

AC Q6J758;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Easily wettable (Fragment) (Fragment).

DE Neurospora sitophila.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OC NCBI_TaxID=40126;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=P8085;

RC Winefield R.D., Beaver R.E., Newcomb R.D., Haverkamp R.G.,

RA Templeton M.D.;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY577557; AAT39533.1; -.

DR EMBL; AY577550; AAT40751.1; -.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0005199; F:structural constituent of cell wall; IEA.

DR InterPro; IPR001338; Hydrophobin.

DR Pfam; PF01185; Hydrophobin; 1.

DR SMART; SMO0075; HYDRO; 1.

DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1.

FT NON_TER 1 1

FT NON_TER 91 91

SQ SEQUENCE 91 AA; 9095 MW; EE02886C772C0220 CRC64;

Query Match 44.0%; Score 51; DB 2; Length 91;

Best Local Similarity 72.7%; Pred. No. 2.5;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CCNDNTVTNTAN 20

DB 77 CCKDDVTNTGN 87

RESULT 5

Q6J763 PRELIMINARY; PRT; 91 AA.

AC Q6J763;

AC Q6J763;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Easily wettable (Fragment).

DE Neurospora discreta.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OC NCBI_TaxID=29879;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=Kirbyville-6;

RC Winefield R.D., Beaver R.E., Newcomb R.D., Haverkamp R.G.,

RA Templeton M.D.;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY577551; AAT40752.1; -.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0005199; F:structural constituent of cell wall; IEA.

DR InterPro; IPR001338; Hydrophobin.

DR Pfam; PF01185; Hydrophobin; 1.

DR SMART; SMO0075; HYDRO; 1.

DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1.

FT NON_TER 1 1

FT NON_TER 91 91

SQ SEQUENCE 91 AA; 9076 MW; 17610899D7CB8FEA CRC64;

Query Match 44.0%; Score 51; DB 2; Length 91;

Best Local Similarity 72.7%; Pred. No. 2.5;

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Query Match 44.0%; Score 51; DB 2; Length 91;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 CCNDNVNTNTAN 20
|||:|||||
Db 77 CKKDDVTNTGN 87

RESULT 8
ID Q6J768 PRELIMINARY; PRT; 91 AA.
AC Q6J768;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Easily wettable (Fragment).
OS Neurospora intermedia.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Taipai-1c;
RA Winefield R.D.; Beaver R.E., Newcomb R.D., Haverkamp R.G.,
RA Templetton M.D.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY575456; AAT40747.1; -.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
DR InterPro; IPR001338; Hydrophobin.
DR Pfam; PF01185; Hydrophobin; 1.
DR SMART; SM00075; HYDRO; 1.
DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 9063 MW; 00DB476C6D8460EA CRC64;

Query Match 44.0%; Score 51; DB 2; Length 91;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 CCNDNVNTNTAN 20
|||:|||||
Db 77 CKKDDVTNTGN 87

RESULT 8
ID Q6J769 PRELIMINARY; PRT; 91 AA.
AC Q6J769;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Easily wettable (Fragment).
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=St. Lawrence Sta;
RA Winefield R.D.; Beaver R.E., Newcomb R.D., Haverkamp R.G.,
RA Templetton M.D.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY575455; AAT40746.1; -.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
DR InterPro; IPR001338; Hydrophobin.
DR Pfam; PF01185; Hydrophobin; 1.
DR SMART; SM00075; HYDRO; 1.
DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 9063 MW; 00DB476C6D8460EA CRC64;

Query Match 44.0%; Score 51; DB 2; Length 91;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 CCNDNVNTNTAN 20
|||:|||||
Db 77 CKKDDVTNTGN 87

RESULT 9
ID Q6J769 PRELIMINARY; PRT; 91 AA.
AC Q6J769;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Easily wettable (Fragment).
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=St. Lawrence Sta;
RA Winefield R.D.; Beaver R.E., Newcomb R.D., Haverkamp R.G.,
RA Templetton M.D.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY575455; AAT40746.1; -.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
DR InterPro; IPR001338; Hydrophobin.
DR Pfam; PF01185; Hydrophobin; 1.
DR SMART; SM00075; HYDRO; 1.
DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 9063 MW; 00DB476C6D8460EA CRC64;

Query Match 44.0%; Score 51; DB 2; Length 91;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 CCNDNVNTNTAN 20
|||:|||||
Db 77 CKKDDVTNTGN 87

RESULT 10
ID Q6J769 PRELIMINARY; PRT; 108 AA.
AC Q6J769;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Hydrophobin precursor (Rodlet protein) (Clock-controlled gene protein
DE 2) (Blue light induced protein 7).
GN Name=eas; Synonyms=bli-7, ccg-2; ORFNames=NCU08457.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93093471; PubMed=1459459;
RX Lauter F.-R., Russo V.E.A., Yanofsky C.;
RA "Developmental and light regulation of eas, the structural gene for
RT the rodlet protein of Neurospora.";
RL Genes Dev. 6:2373-2381 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=93093472; PubMed=1459460;
RA Bell-Pedersen D., Dunlap J.C., Loros J.J.;
RT "The Neurospora circadian clock-controlled gene, ccg-2, is allelic to
RT eas and encodes a fungal hydrophobin required for formation of the
RT conidial rodlet layer.";
RL Genes Dev. 6:2382-2394 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=93112994; PubMed=1472707;
RA Eberle J., Russo V.E.A.;
RT "Neurospora crassa blue-light-inducible gene bli-7 encodes a short
RT hydrophobic protein.";
RL DNA Seq. 3:131-141 (1992).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamyselis M.,
RA Mauceli E., Bielke C., Rudd S., Frisman D., Krystofova S.,
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macosko C.P., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868 (2003).
CC -!- FUNCTION: Contributes to surface hydrophobicity, which is
CC important for processes such as association of hyphae in
```

DR	PTIR; D34027; VCLJB4.
DR	InterPro; IPR001027; Gp45_EIAY.
DR	Pfam; PFO01361; Gp90_EIAY.
DR	Pfam; PF01045; EIAY_GP45; 1.
DR	Pfam; PR00971; EIAY_GP90; 1.
KW	Coat protein; Glycoprotein; Polyprotein; Signal; Transmembrane.
FT	SIGNAL 1 22 Potential.
FT	CHAIN 23 860 Env polyprotein.
FT	CHAIN 23 445 Coat protein GP90.
FT	CHAIN 446 860 Coat protein GP45.
FT	TRANSMEM 75 93 Potential.
FT	TRANSMEM 447 463 Potential.
FT	TRANSMEM 615 637 Potential.
FT	TRANSMEM 788 808 Potential.
FT	TRANSMEM 817 836 Potential.
FT	CARBOHYD 40 40 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 112 112 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 214 214 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 235 235 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 308 308 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 337 337 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 340 340 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 346 346 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 400 400 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 407 407 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 412 412 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 491 491 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 551 551 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 558 558 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 753 753 N-linked (GlcNAc...) (Potential).
SQ	SEQUENCE 860 AA; 97020 MW; 0037EB61528EF0DD CRC64;
Query Match 44.0%; Score 51; DB 1; Length 860;	
Best Local Similarity 44.4%; Pred. No. 26;	
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps	
QY	1 KENSAPPFPCNDNVNT 18 ::: :
Db	28 EENTFPQCYNNNSQS 45
RESULT 12	
Q6AXF9	PRELIMINARY; PRT; 863 AA.
ID	O6AXF9
AC	O6AXF9
DT	23-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Sez612 protein.
GN	Name=Sez612;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON	NCBI_TaxID=10090;
OX	[1]
RP	SEQUENCE FROM N.A.
RC	STRAN=C57BL/6; TISSUE=Brain;
RX	PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Brain;
RC Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079573; AAH79573.1; -
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; Sush1; 5.
DR SMART; SM00032; CCP; 5.
DR SMART; SMO0042; CUB; 3.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS50923; SUSH1; 5.
SQ SEQUENCE 363 AA; 93371 MW; 82AC231639C0EB75 CRC64;
Query Match 44.0%; Score 51; DB 2; Length 863;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 KENSAPPPFCNDVNTVT 18
Db :|: ||||| : |||||
400 EEDRCPPFLAHGNVTT 417
RESULT 13
Q91X64
ID Q91X64 PRELIMINARY; PRT; 923 AA.
AC Q91X64;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Seizure related 6 homolog (Mouse)-like 2 (Mus musculus adult male
DE dienecephalon cDNA, RIKEN full-length enriched library,
DE clone:933015G24 product:TYPE I TRANSMEMBRANE RECEPTOR homolog).
GN Name=Sez612;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Brain;
RC Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079573; AAH79573.1; -
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; Sush1; 5.
DR SMART; SM00032; CCP; 5.
DR SMART; SMO0042; CUB; 3.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS50923; SUSH1; 5.
SQ SEQUENCE 363 AA; 93371 MW; 82AC231639C0EB75 CRC64;

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Salivary gland;
RC Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh A.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-394-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Brain;
RC Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079573; AAH79573.1; -
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; Sush1; 5.
DR SMART; SM00032; CCP; 5.
DR SMART; SMO0042; CUB; 3.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS50923; SUSH1; 5.
SQ SEQUENCE 363 AA; 93371 MW; 82AC231639C0EB75 CRC64;

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.

DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00084; Sushi; 5.
 DR SMART; SM00032; CCP; 5.
 DR SMART; SM00042; CUB; 3.
 DR PROSITE; PS01180; CUB; 3.
 DR PROSITE; PS03023; SUSHI; 5.
 DR Receptor; Transmembrane.
 SK SEQUENCE 923 AA; 99077 MW; DD15A1DF50848889 CRC64;

Query Match 44.0%; Score 51; DB 2; Length 923;
 Best Local Similarity 50.0%; Pred. No. 28;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 KENSAPPPPCNDNVNT 18

Db 460 EEDRCFPFLAHGNVTT 477

RESULT 14

Q6J765

ID Q6J765 PRELIMINARY; PRT; 91 AA.

AC Q6J765;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Easily wettable (Fragment).

OS Neurospora tetrasperma.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=40127;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=CBS 259.35;

RA Winefield R.D.; Beever R.E.; Newcomb R.D.; Haverkamp R.G.;

RA Templeton M.D.;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY57549; AAT0750.1;

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0005199; F:structural constituent of cell wall; IEA.

DR InterPro; IPR001338; Hydrophobin.

DR Pfam; PF01185; Hydrophobin; 1.

DR SMART; SM00075; HYDRO; 1.

DR PROSITE; PS00956; HYDROPHOBIN; UNKNOWN_1.

FT NON_TER 1 91

FT NON_TER 91 91

SQ SEQUENCE 91 AA; 9005 MW; ODD844A36D8460EA CRC64;

Query Match

Best Local Similarity 43.1%; Score 50; DB 2; Length 91;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 CCNDNVNTAN 20

Db 77 CCKDGVNTGN 87

RESULT 15

Q99J59

ID Q99J59 PRELIMINARY; PRT; 240 AA.

AC Q99J59;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE RIKEN cDNA 9030418M05 (Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030418M05 product:similar to tetraspan

DE TSPAN-1).

GN Name=9030418M05Rik;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN

RP SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

RA Altshul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh P.;

RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;

RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

RA Bobak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

RA Richards S.; Worley K.C.; Hale S.A.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

RA Fahy J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.;

RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;

RA Krzywinski M.I.; Skalska U.; Smailus D.E.; Schnerch A.; Schein J.E.;

RA Jones S.J.; Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=Mammary tumor;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

[3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P.; Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

[5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon;

RA The FANTOM Consortium;

RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

[6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;

RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

[7]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Colon;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K.; Itoh M.; Aizawa K.; Nagaoka S.; Sasaki N.; Carninci P.;

RA Konno H.; Akiyama J.; Nishi K.; Kitsuai T.; Tashiro H.; Itoh M.;

RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;

RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;

RA Fujiwaki S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watanaki M.;

RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai J.;

RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

```
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Iehi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamanura T., Yamanaka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003448; AAH03448.1; -.
DR MGD; MGI:1914055; 9030418M05Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR008952; Tetraspanin.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00342; RHEUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
SQ SEQUENCE 240 AA; 26356 MW; AD4C48A32BC2999 CRC64;

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Best Local Similarity 72.7%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db ||| ||| |||
165 KENKVFPPFCC 175
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